

GTTTAGTCTGCAGCCGAGCAGCTAAAGGGAGAAAGAATCGCTCAGGAAAGACACACTGCAGACTCCACGGCACCCCTGC	79
AATAGATGGGTTCCGACTACACAAAGGAGAAAACCGGAGGTGACACTCTCCTGCCCTGGAAGAGGACGAAACGACCAA	158
CAAACGCAAGGACTGGACTCCATGCCGAAGGTATCTGGAAGTCGTGACACCGTGTGTATATAACAAAAGTTTGCGAGCT	237
GTTAATTGCTGTGCTGTATTAAAGAGACGCTTTCAAGTTTCAAGTACCAAAATGTAGCTTTACGTTGCCAAAGGAAGT	316
TGAGGCAATTGCTTTGCTGTTTAACTTGCTCTGTGAGGAAATCTCATAAACTGACCA ATG CAC CAA ATG AAT	5- 390
A K M H F R F V F A L L I V S F N H D V	25
GCT AAA ATG CAC TTT AGG TTT GTT TTT GCA CTT CTG ATA GTA TCT TTC AAC CAC GAT GTA	450
L G K N L K Y R I Y E E Q R V G S V I A	45
CTG GGC AAG AAT TTG AAA TAC AGG ATT TAT GAG GAA CAG AGG GTT GGA TCA GTA ATT GCA	510
R L S E D V A D V L L L K L P N P S T V R	65
AGA CTA TCA GAG GAT GTG GCT GAT GTT TTA TTG AAG CTT CCT AAT CCT TCT ACT GTT CGA	570
F R A M Q R G N S P L L L V V N E D N G E	85
TTT CGA GCC ATG CAG AGG GGA AAT TCT CCT CTA CTT GTA GTA AAC GAG GAT AAT GGG GAA	630

Fig. 1A

I	S	I	G	A	T	I	D	R	E	Q	L	C	Q	K	N	L	N	C	S	105	
ATC	AGC	ATA	GGG	GCT	ACA	ATT	GAC	CGT	GAA	CAA	CTG	TGC	TGC	CAG	AAA	AAC	TTG	AAC	TGT	TCC	690
I	E	F	D	V	I	T	L	P	T	E	H	L	Q	L	F	H	I	E	V	125	
ATA	GAG	TTT	GAT	GTG	ATC	ACT	CTA	CCC	ACA	GAG	CAT	CTG	CAG	CTT	TTC	CAT	ATT	GAA	GTT	750	
E	V	L	D	I	N	D	N	S	P	Q	F	S	R	S	L	I	P	I	E	145	
GAA	GTG	CTG	GAT	ATT	AAT	GAC	AAT	TCT	CCC	CAG	TTT	TCA	AGA	TCT	CTC	ATA	CCT	ATT	GAG	810	
I	S	E	S	A	A	V	G	T	R	I	P	L	D	S	A	F	D	P	D	165	
ATA	TCT	GAG	AGT	GCA	GCA	GTT	GGG	ACT	CGC	ATT	CCC	CTG	GAC	AGT	GCA	TTT	GAT	CCA	GAT	870	
V	G	E	N	S	L	H	T	Y	S	L	S	A	N	D	F	F	N	I	E	185	
GTT	GGG	GAA	AAT	TCC	CTC	CAC	ACA	TAC	TCG	CTC	TCT	GCC	AAT	GAT	TTT	TTT	AAT	ATC	GAG	930	
V	R	T	R	T	D	G	A	K	Y	A	E	L	I	V	V	R	E	L	D	205	
GTT	CGG	ACC	AGG	ACT	GAT	GGA	GCC	AAG	TAT	GCA	GAA	CTC	ATA	GTG	GTC	AGA	GAG	TTA	GAT	990	
R	E	L	K	S	S	Y	E	L	Q	L	T	A	S	D	M	G	V	P	Q	225	
CGG	GAG	CTG	AAG	TCA	AGC	TAC	GAG	CTT	CAG	CTC	ACT	GCC	TCA	GAC	ATG	GGA	GTA	CCT	CAG	1050	
R	S	G	S	S	I	L	K	I	S	I	S	D	S	N	D	N	S	P	A	245	
AGG	TCT	GGC	TCA	TCC	ATA	CTA	AAA	ATA	AGC	ATT	TCA	GAC	TCC	AAT	GAC	AAC	AGC	CCT	GCT	1110	

**Fig. 1B**

F	E	Q	Q	S	Y	I	I	I	Q	L	L	L	E	N	S	P	V	G	T	L	L	265
TTT	GAG	CAG	CAA	TCT	TAT	ATA	ATA	ATA	CAA	CTC	TTA	GAA	AAC	TCC	CCG	GTT	GGC	ACT	TTG	CTC	1170	
L	D	L	N	A	T	D	P	D	P	D	E	G	A	N	G	K	I	V	Y	S	F	285
TTA	GAT	CTG	AAT	GCC	ACG	GAT	CCA	GAT	CCA	GAT	GAG	GGC	GCT	AAT	GGG	AAA	ATT	GTA	TAT	TCC	TTT	1230
S	S	H	V	S	P	K	I	M	I	M	E	T	F	K	I	D	S	E	R	G	H	305
AGC	AGT	CAT	GTG	TCT	CCC	AAA	ATT	ATG	ATG	GAG	ACT	TTT	AAA	ATT	GAT	TCT	GAA	AGA	GGA	CAT	1290	
L	T	L	F	K	Q	V	D	Y	E	I	T	K	S	Y	E	I	D	V	Q	325		
TTG	ACT	CTT	TTC	AAG	CAA	GTG	GAT	TAT	GAA	ATC	ACC	AAA	TCC	TAT	GAG	ATT	GAT	GTT	CAG	1350		
A	Q	D	L	G	P	N	S	I	P	A	H	C	K	I	I	I	K	V	V	345		
GCT	CAA	GAT	TTG	GGT	CCA	AAT	TCA	ATC	CCA	GCC	CAT	TGC	AAA	ATT	ATA	ATT	AAG	GTT	GTG	1410		
D	V	N	D	N	K	P	E	I	N	I	N	L	M	S	P	G	K	E	E	365		
GAT	GTT	AAT	GAC	AAT	AAA	CCT	GAA	ATT	AAC	ATC	AAC	CTC	ATG	TCC	CCT	GGA	AAA	GAA	GAA	1470		
I	S	Y	I	F	E	G	D	P	I	D	T	F	V	A	L	V	R	V	Q	385		
ATA	TCT	TAT	ATT	TTT	GAA	GGG	GAT	CCT	ATT	GAT	ACA	TTT	GTT	GCT	TTG	GTC	AGA	GTT	CAG	1530		
D	K	D	S	G	L	N	G	E	I	V	C	K	L	H	G	H	G	H	F	405		
GAC	AAG	GAT	TCT	GGG	CTG	AAT	GGA	GAA	ATA	GTT	TGT	AAG	CTT	CAT	GGA	CAT	GGT	CAC	TTT	1590		

**Fig. 1C**

K	L	Q	CAG	AAG	ACA	TAT	GAA	AAC	AAT	TAT	TTA	ATC	TTA	ACT	TAA	CTG	GAT	AGA	425	
AAA	CTT	CAG	AAG	ACA	TAT	GAA	AAC	AAT	TAT	TTA	ATC	TTA	ACT	TAA	CTG	GAT	AGA	1650		
E	K	R	AGA	TCT	GAG	TAT	AGT	TTG	ACT	GTA	ATC	GCT	GAG	GAC	AGG	GCG	ACA	CCC	445	
GAA	AAG	AGA	TCT	GAG	TAT	AGT	TTG	ACT	GTA	ATC	GCT	GAG	GAC	AGG	GCG	ACA	CCC	AGT	1710	
S	T	V	K	H	F	T	V	Q	I	N	D	I	N	D	N	P	P	H	F	465
TCT	ACA	GTG	AAA	CAT	TTT	ACA	GTT	CAA	ATC	AAT	GAT	ATC	AAT	GAC	AAT	CCA	CCC	CAC	1770	
Q	R	S	R	Y	E	F	V	I	S	E	N	N	N	S	P	G	A	Y	I	485
CAG	AGA	AGC	CGA	TAT	GAA	TTT	GTA	ATT	TCA	GAA	AAT	AAC	TCA	CCA	GCG	GCA	TAT	ATC	1830	
T	V	T	A	T	D	P	D	L	G	E	N	G	Q	V	T	Y	T	I	L	505
ACT	GTT	ACA	GCC	ACA	GAT	CCT	GAT	CTT	GGA	GAA	AAT	GCG	CAA	GTG	ACA	TAC	ACC	ATC	1890	
E	S	F	I	L	G	S	S	I	T	Y	V	T	I	D	P	S	N	G	G	525
GAG	AGT	TTT	ATT	CTA	GGA	AGT	TCC	ATA	ACT	ACA	TAT	GTA	ACC	ATT	GAC	CCA	TCT	AAT	1950	
A	I	Y	A	L	R	I	F	D	H	E	E	V	S	Q	I	T	F	V	V	545
GCC	ATC	TAT	GCC	CTC	AGA	ATC	TTT	GAT	CAT	GAA	GAA	GTG	AGT	CAG	ATC	ACT	TTT	GTG	2010	
E	A	R	D	G	G	S	P	K	Q	L	V	S	N	T	T	V	V	L	T	565
GAA	GCA	AGA	GAT	GGA	GGA	AGC	CCG	AAG	CAA	CTG	GTA	AGC	AAT	ACC	ACA	GTT	GTG	CTC	2070	

**Fig. 1D**



I	I	D	E	N	D	N	V	P	V	V	I	G	P	A	L	R	N	N	T	585
ATC	ATT	GAC	GAA	AAT	GAC	AAC	GTT	CCT	GTG	GTT	ATA	GGG	CCT	GCA	TTG	CGT	AAT	AAT	ACG	2130
A	E	I	T	I	P	K	G	A	E	S	G	F	H	V	T	R	I	R	A	605
GCA	GAA	ATC	ACC	ATT	CCC	AAA	GGG	GCT	GAA	AGT	GGC	TTT	CAT	GTC	ACA	AGA	ATA	AGG	GCA	2190
I	D	R	D	S	G	V	N	A	E	L	S	C	A	I	V	A	G	N	E	625
ATT	GAC	AGA	GAC	TCT	GGT	GTG	AAT	GCT	GAA	CTC	AGC	TGC	GCC	ATA	GTA	GCA	GGT	AAT	GAG	2250
E	N	I	F	I	I	D	P	R	S	C	D	I	H	T	N	V	S	M	D	645
GAG	AAT	ATC	TTC	ATA	ATT	GAT	CCA	CGA	TCA	TGT	GAC	ATC	CAT	ACC	AAC	GTT	AGC	ATG	GAT	2310
S	V	P	Y	T	E	W	E	L	S	V	I	I	Q	D	K	G	N	P	Q	665
TCT	GTT	CCC	TAC	ACA	GAA	TGG	GAG	CTG	TCA	GTT	ATC	ATT	CAG	GAC	AAA	GGC	AAT	CCT	CAG	2370
L	H	T	K	V	L	L	K	C	M	I	F	E	Y	A	E	S	V	T	S	685
CTA	CAT	ACC	AAA	GTC	CTT	CTG	AAG	TGC	ATG	ATC	TTT	GAA	TAT	GCA	GAG	TCG	GTG	ACA	AGT	2430
T	A	M	T	S	V	S	Q	A	S	L	D	V	S	M	I	I	I	I	S	705
ACA	GCA	ATG	ACT	TCA	GTA	AGC	CAG	GCA	TCC	TTG	GAT	GTC	TCC	ATG	ATA	ATA	ATT	ATT	TCC	2490
L	G	A	I	C	A	V	L	L	V	I	M	V	L	F	A	T	R	C	N	725
TTA	GGA	GCA	ATT	TGT	GCA	GTG	TTG	CTG	GTT	ATT	ATG	GTG	CTA	TTT	GCA	ACT	AGG	TGT	AAC	2550

**Fig. 1E**

R	E	K	K	D	T	R	S	Y	N	C	R	V	A	E	S	T	Y	Q	H	745
CGC	GAG	AAG	AAA	GAC	ACT	AGA	TCC	TAT	AAC	TGC	AGG	GTG	GCC	GAA	TCA	ACT	TAC	CAG	CAC	2610
H	P	K	R	P	S	R	Q	I	H	K	G	D	I	T	L	V	P	T	I	765
CAC	CCA	AAA	AGG	CCA	TCC	CGG	CAG	ATT	CAC	AAA	GGG	GAC	ATC	ACA	TTG	GTG	CCT	ACC	ATA	2670
N	G	T	L	P	I	R	S	H	H	R	S	S	P	S	S	S	P	T	L	785
AAT	GGC	ACT	CTG	CCC	ATC	AGA	TCT	CAT	CAC	AGA	TCG	TCT	CCA	TCT	TCA	TCT	CCT	ACC	TTA	2730
E	R	G	Q	M	G	S	R	Q	S	H	N	S	H	Q	S	L	N	S	L	805
GAA	AGA	GGG	CAG	ATG	GGC	AGC	CGG	CAG	AGT	CAC	AAC	AGT	CAC	CAG	TCA	CTC	AAC	AGT	TTG	2790
V	T	I	S	S	N	H	V	P	E	N	F	S	L	E	L	T	H	A	T	825
GTG	ACA	ATC	TCA	TCA	AAC	CAC	GTG	CCA	GAG	AAT	TTC	TCA	TTA	GAA	CTC	ACC	CAC	GCC	ACT	2850
P	A	V	E	Q	V	S	Q	L	L	S	M	L	H	Q	G	Q	Y	Q	P	845
CCT	GCT	GTT	GAG	CAG	GTC	TCT	CAG	CTT	CTT	TCA	ATG	CTT	CAC	CAG	GGG	CAA	TAT	CAG	CCA	2910
R	P	S	F	R	G	N	K	Y	S	R	S	Y	R	Y	A	L	Q	D	M	865
AGA	CCA	AGT	TTT	CGA	GGA	AAC	AAA	TAT	TCC	AGG	AGC	TAC	AGA	TAT	GCC	CTT	CAA	GAC	ATG	2970
D	K	F	S	L	K	D	S	G	R	G	D	S	E	A	G	D	S	D	Y	885
GAC	AAA	TTT	AGC	TTG	AAA	GAC	AGT	GGC	CGT	GGT	GAC	AGT	GAG	GCA	GGA	GAC	AGT	GAT	TAT	3030

**Fig. 1F**

D	L	G	R	D	S	P	I	D	R	L	L	G	E	G	F	S	D	L	F	905
GAT	TTG	GGG	CGA	GAT	TCT	CCA	ATA	GAT	AGG	CTG	CTG	GGT	GAA	GGA	TTC	AGC	GAC	CTG	TTT	3090
L	T	D	G	R	I	P	A	A	M	R	L	C	T	E	E	C	R	V	L	925
CTC	ACA	GAT	GGA	AGA	ATT	CCA	GCA	GCT	ATG	AGA	CTC	TGC	ACG	GAG	GAG	TGC	AGG	GTC	CTG	3150
G	H	S	D	Q	C	W	M	P	P	L	P	S	P	S	S	D	Y	R	S	945
GGA	CAC	TCT	GAC	CAG	TGC	TGG	ATG	CCA	CCA	CTG	CCC	TCA	CCG	TCT	TCT	GAT	TAT	AGG	AGT	3210
N	M	F	I	P	G	E	E	F	P	T	Q	P	Q	Q	Q	H	P	H	Q	965
AAC	ATG	TTC	ATT	CCA	GGG	GAA	GAA	TTC	CCA	ACG	CAA	CCC	CAG	CAG	CAG	CAT	CCA	CAT	CAG	3270
S	L	E	D	D	A	Q	P	A	D	S	G	E	K	K	K	S	F	S	T	985
AGT	CTT	GAG	GAT	GAC	GCT	CAG	CCT	GCA	GAT	TCC	GGT	GAA	AAG	AAG	AAG	AGT	TTT	TCC	ACC	3330
F	G	K	D	S	P	N	D	E	D	T	G	D	T	S	T	S	S	L	L	1005
TTT	GGA	AAG	GAC	TCC	CCA	AAC	GAT	GAG	GAC	ACT	GGG	GAT	ACC	AGC	ACA	TCA	TCT	CTG	CTC	3390
S	E	M	S	S	V	F	Q	R	L	L	P	P	S	L	D	T	Y	S	E	1025
TCG	GAA	ATG	AGC	AGT	GTG	TTC	CAG	CGT	CTC	TTA	CCG	CCT	TCC	CTG	GAC	ACC	TAT	TCT	GAA	3450
C	S	E	V	D	R	S	N	S	L	E	R	R	K	G	P	L	P	A	K	1045
TGC	AGT	GAG	GTG	GAT	CGG	TCC	AAC	TCC	CTG	GAG	CGC	AGG	AAG	GGA	CCC	TTG	CCA	GCC	AAA	3510

**Fig. 1G**

T	V	G	Y	P	Q	G	V	A	A	W	A	A	S	T	H	F	Q	N	P	1065			
ACT	GTG	GGT	TAC	CCA	CAG	GGG	GTA	GCG	GCA	TGG	GCA	GCC	AGT	ACG	CAT	TTT	CAA	AAT	CCC	3570			
T	T	N	C	G	P	P	L	G	T	H	S	S	V	Q	P	S	S	K	W	1085			
ACC	ACC	AAC	TGT	GGG	CCG	CCA	CTT	GGA	ACT	CAC	TCC	AGT	GTG	CAG	CCT	TCT	TCA	AAA	TGG	3630			
L	P	A	M	E	E	I	P	E	N	Y	E	E	D	D	F	D	N	V	L	1105			
CTG	CCA	GCC	ATG	GAG	GAG	ATC	CCT	GAA	AAT	TAT	GAG	GAA	GAT	GAT	TTT	GAC	AAT	GTG	CTC	3690			
N	H	L	N	D	G	K	H	E	L	M	D	A	S	E	L	V	A	E	I	1125			
AAC	CAC	CTC	AAT	GAT	GGG	AAA	CAC	GAA	CTC	ATG	GAT	GCC	AGT	GAA	CTG	GTG	GCA	GAG	ATT	3750			
N	K	L	L	Q	D	V	R	Q	S	*											1135		
AAC	AAA	CTG	CTT	CAA	GAT	GTC	CGC	CAG	AGC	TAG											3783		
GAG	ATTTAG	CGAAG	CA	TTTTTT	GTTC	CATGT	ATAT	TGG	AAATAG	GGAA	CAACA	CAACA	CAACA	CAACA	CAACA	CAACA	CAACA	CAACA	CAACA	3862			
TGG	CATTG	CCAAA	TAG	TG	CA	TTTAT	CA	TAA	TG	CTG	TAT	ATTG	AA	TAT	TAA	TACT	GT	ATTT	TCGT	ATGTACA	3941		
CA	TGCA	AGT	GTG	AT	TTTAA	CTG	AT	TTTAA	AAATAC	ATTTG	TAC	CTTAT	AT	TTTAT	TG	TAA	TTTAA	CAACA	CAACA	4020			
TTT	TAT	TTTT	TACT	CCCA	TG	ACAG	ACAT	GT	TTTCC	TAG	TCGT	AGAA	CA	TTAG	CCCA	CTG	TCAA	ATCT	GATAC	ACTA	4099		
TT	CA	ACC	CA	AG	TG	TAA	GGC	ACT	G	CTT	AG	TTT	TG	TGG	GA	AGAA	TTAT	TG	TG	TATGA	CAAC	4178	
GA	GC	ATT	AT	CTT	AA	TTCC	AT	TA	AG	TG	ATCC	CA	CTT	TTT	TCA	ATA	AC	TTTT	TAG	AAAT	TAAG	AAATCA	4257
AT	TG	TA	AG	CT	AT	TTT	AT	TTT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	4336
TAA	AG	TAA	AG	TTT	AT	TTT	AT	TTT	AT	TTT	AT	TTT	AT	TTT	AT	TTT	AT	TTT	AT	TTT	AT	TTT	4415

**Fig. 1H**

AGACAAATGATGAAACAGAACTAAAGTCAATGTTTCCTGACTCCCAGGCCCCCTACTATTCCAGGCCATCACACTGGCCT 4494  
 GTTCCGGAGAATATTTCTCTCACAAATATTAATCTACTTATAATATGGTAAACAATAAAATTTTATTCCATCCTTGTA 4573  
 GTATGAAACATGCTCCAGGAAATGGAATCTGTCCCTTAAATGGATAACAGTATGTGTTCTAAATGGCATAAAAATATTAC 4652  
 TGGATAAAACAGTTGTGTCAGTGTCTCCTAAGGTAGTAAATAATAATTGACTTATTCTGAACCCATTCTATTTTGAA 4731  
 TCTCCCCCTTCTCCATACATACTTGAACATTTTAATCTTTTGGAAATATTGCTCTTCTTTGTTATAAACTATTCAATTTT 4810  
 AGCTTTTGTCCTCCAGTGCAATGATCTCATATTTTGGCTTTTATTTTAGTATAAGAACATTTATATAAAATCATATTTTGT 4889  
 TACTGCAATTGTTTATTTGTTGTGGCAAAATGAGAAAATCCCTTTATTTATTGTGCTGTGATCTCTCTGTGGAAATGC 4968  
 CTTGGTGAGAGAGATGCTTATTATGACTATTATCATTTCTGACCAAGCTTCTATTAAATGTTATTCTTAATAATACACTA 5047  
 TCTTGATTGTACTCTCCAGAAAAATTTTCTGTCTCAGTGAAAAATAAAGAAAAATTAAGTAAAAAATAAAAAA 5121

**Fig. 11**

GTTAGTCTGCAGCCGAGCAGCTAAAGGAGAAAGAAATCGCTCAGGAAAGACACACTGCAGACTCCACCGCACCCCTGC	79
AATAGATGGTTCCGACTACACAAGGGAGAAACCGGAGGTGACACTCTCCTGCCTGGAAAGAGGACGAAACGACCAA	158
CAAACGCAAGGACTGGACTCCATGCCGAAGGTATCTGGAAGTCGTGACACCGTGTGTATATAAACAAAAGTTTCCGAGCT	237
GTTAATTCGTGCTGTGTATTATAAGAGACGCTTTCAGGTTTCAAGTTTCAAGTACCAAAATGTAGCTTTACGTTGCCAAAGGAAAGT	316
M H Q M N	
TGAGGCAATTGCTTTGCTGTTTAACTTGCTCTGTGAGGAAATCTCATAAACTGACCA ATG CAC CAA ATG AAT	5 390
A K M H F R F V F A L L I V S F N H D V	25
GCT AAA ATG CAC TTT AGG TTT GTT TTT GCA CTT CTG ATA GTA TCT TTC AAC CAC GAT GTA	450
L G K N L K Y R I Y E E Q R V G S V I A	45
CTG GGC AAG AAT TTG AAA TAC AGG ATT TAT GAG GAA CAG AGG GTT GGA TCA GTA ATT GCA	510
R L S E D V A D V L L L K L P N P S T V R	65
AGA CTA TCA GAG GAT GTG GCT GAT GTT TTA TTG AAG CTT CCT AAT CCT TCT ACT GTT CGA	570
F R A M Q R G N S P L L L V V N E D N G E	85
TTT CGA GCC ATG CAG AGG GGA AAT TCT CCT CTA CTT GTA GTA AAC GAG GAT AAT GGG GAA	630
I S I G A T I D R E Q L C Q K N L N C S	105
ATC AGC ATA GGG GCT ACA ATT GAC CGT GAA CAA CTG TGC CAG AAA AAC TTG AAC TGT TCC	690

**Fig. 2A**

I	E	F	D	V	I	T	L	P	T	E	H	L	Q	L	F	H	I	E	V	125
ATA	GAG	TTT	GAT	GTG	ATC	ACT	CTA	CCC	ACA	GAG	CAT	CTG	CAG	CTT	TTC	CAT	ATT	GAA	GTT	750
E	V	L	D	I	N	D	N	S	P	Q	F	S	R	S	L	I	P	I	E	145
GAA	GTG	CTG	GAT	ATT	AAT	GAC	AAT	TCT	CCC	CAG	TTT	TCA	AGA	TCT	CTC	ATA	CCT	ATT	GAG	810
I	S	E	S	A	A	V	G	T	R	I	P	L	D	S	A	F	D	P	D	165
ATA	TCT	GAG	AGT	GCA	GCA	GTT	GGG	ACT	CGC	ATT	CCC	CTG	GAC	AGT	GCA	TTT	GAT	CCA	GAT	870
V	G	E	N	S	L	H	T	Y	S	L	S	A	N	D	F	F	N	I	E	185
GTT	GGG	GAA	AAT	TCC	CTC	CAC	ACA	TAC	TCG	CTC	TCT	GCC	AAT	GAT	TTT	TTT	AAT	ATC	GAG	930
V	R	T	R	T	D	G	A	K	Y	A	E	L	I	V	V	R	E	L	D	205
GTT	CGG	ACC	AGG	ACT	GAT	GGA	GCC	AAG	TAT	GCA	GAA	CTC	ATA	GTG	GTC	AGA	GAG	TTA	GAT	990
R	E	L	K	S	S	Y	E	L	Q	L	T	A	S	D	M	G	V	P	Q	225
CGG	GAG	CTG	AAG	TCA	AGC	TAC	GAG	CTT	CAG	CTC	ACT	GCC	TCA	GAC	ATG	GGA	GTA	CCT	CAG	1050
R	S	G	S	S	I	L	K	I	S	I	S	D	S	N	D	N	S	P	A	245
AGG	TCT	GGC	TCA	TCC	ATA	CTA	AAA	ATA	AGC	ATT	TCA	GAC	TCC	AAT	GAC	AAC	AGC	CCT	GCT	1110
F	E	Q	Q	S	Y	I	I	Q	L	L	E	N	S	P	V	G	T	L	L	265
TTT	GAG	CAG	CAA	TCT	TAT	ATA	ATA	CAA	CTC	TTA	GAA	AAC	TCC	CCG	GTT	GGC	ACT	TTG	CTC	1170

**Fig. 2B**

L	D	L	L	N	A	T	D	P	D	E	G	A	N	G	K	I	V	Y	S	F	285	
TTA	GAT	CTG	AAT	GCC	ACG	GAT	CCA	GAT	CCA	GAT	GAG	GCG	GCT	AAT	GGG	AAA	ATT	GTA	TAT	TCC	TTC	1230
S	S	H	V	S	P	K	I	M	E	E	T	F	K	I	D	S	E	R	G	H	305	
AGC	AGT	CAT	GTG	TCT	CCC	AAA	ATT	ATG	GAG	ACT	TTT	AAA	ATT	GAT	TCT	GAA	AGA	GGA	CAT	1290		
L	T	L	F	K	Q	V	D	Y	E	I	T	K	S	Y	E	I	D	V	Q	325		
TTG	ACT	CTT	TTC	AAG	CAA	GTG	GAT	TAT	GAA	ATC	ACC	AAA	TCC	TAT	GAG	ATT	GAT	GTT	CAG	1350		
A	Q	D	L	G	P	N	S	I	P	A	H	C	K	I	I	I	K	V	V	345		
GCT	CAA	GAT	TTG	GGT	CCA	AAT	TCA	ATC	CCA	GCC	CAT	TGC	AAA	ATT	ATA	ATT	AAG	GTT	GTG	1410		
D	V	N	D	N	K	P	E	I	N	I	N	L	M	S	P	G	K	E	E	365		
GAT	GTT	AAT	GAC	AAT	AAA	CCT	GAA	ATT	AAC	ATC	AAC	CTC	ATG	TCC	CCT	GGA	AAA	GAA	GAA	1470		
I	S	Y	I	F	E	G	D	P	I	D	T	F	V	A	L	V	R	V	Q	385		
ATA	TCT	TAT	ATT	TTT	GAA	GGG	GAT	CCT	ATT	GAT	ACA	TTT	GTT	GCT	TTG	GTC	AGA	GTT	CAG	1530		
D	K	D	S	G	L	N	G	E	I	V	C	K	L	H	G	H	G	H	F	405		
GAC	AAG	GAT	TCT	GGG	CTG	AAT	GGA	GAA	ATA	GTT	TGT	AAG	CTT	CAT	GGA	CAT	GGT	CAC	TTT	1590		
K	L	Q	K	T	Y	E	N	N	Y	L	I	L	T	N	A	T	L	D	R	425		
AAA	CTT	CAG	AAG	ACA	TAT	GAA	AAC	AAT	TAT	TTA	ATC	TTA	ACT	AAT	GCC	ACA	CTG	GAT	AGA	1650		

**Fig. 2C**



E	K	R	S	E	Y	S	L	T	V	I	A	E	D	R	G	T	P	S	L	445
GAA	AAG	AGA	TCT	GAG	TAT	AGT	TTG	ACT	GTA	ATC	GCT	GAG	GAC	AGG	GGG	ACA	CCC	AGT	CTC	1710
S	T	V	K	H	F	T	V	Q	I	N	D	I	N	D	N	P	P	H	F	465
TCT	ACA	GTG	AAA	CAT	TTT	ACA	GTT	CAA	ATC	AAT	GAT	ATC	AAT	GAC	AAT	CCA	CCC	CAC	TTC	1770
Q	R	S	R	Y	E	F	V	I	S	E	N	N	S	P	G	A	Y	I	T	485
CAG	AGA	AGC	CGA	TAT	GAA	TTT	GTA	ATT	TCA	GAA	AAT	AAC	TCA	CCA	GGG	GCA	TAT	ATC	ACC	1830
T	V	T	A	T	D	P	D	L	G	E	N	G	Q	V	T	Y	T	I	L	505
ACT	GTT	ACA	GCC	ACA	GAT	CCT	GAT	CTT	GGA	GAA	AAT	GGG	CAA	GTG	ACA	TAC	ACC	ATC	TTG	1890
E	S	F	I	L	G	S	S	I	T	T	Y	V	T	I	D	P	S	N	G	525
GAG	AGT	TTT	ATT	CTA	GGA	AGT	TCC	ATA	ACT	ACA	TAT	GTA	ACC	ATT	GAC	CCA	TCT	AAT	GGA	1950
A	I	Y	A	L	R	I	F	D	H	E	E	V	S	Q	I	T	F	V	V	545
GCC	ATC	TAT	GCC	CTC	AGA	ATC	TTT	GAT	CAT	GAA	GAA	GTG	AGT	CAG	ATC	ACT	TTT	GTG	GTA	2010
E	A	R	D	G	G	S	P	K	Q	L	V	S	N	T	T	V	V	L	T	565
GAA	GCA	AGA	GAT	GGA	GGA	AGC	CCG	AAG	CAA	CTG	GTA	AGC	AAT	ACC	ACA	GTT	GTG	CTC	ACC	2070
I	I	D	E	N	D	N	V	P	V	V	I	G	P	A	L	R	N	N	T	585
ATC	ATT	GAC	GAA	AAT	GAC	AAC	GTT	CCT	GTG	GTT	ATA	GGG	CCT	GCA	TTG	CGT	AAT	AAT	ACG	2130

**Fig. 2D**

A	E	I	T	I	P	K	G	A	E	S	G	F	H	V	T	R	I	R	A	605
GCA	GAA	ATC	ACC	ATT	CCC	AAA	GGG	GCT	GAA	AGT	GGC	TTT	CAT	GTC	ACA	AGA	ATA	AGG	GCA	2190
I	D	R	D	S	G	V	N	A	E	L	S	C	A	I	V	A	G	N	E	625
ATT	GAC	AGA	GAC	TCT	GGT	GTG	AAT	GCT	GAA	CTC	AGC	TGC	GCC	ATA	GTA	GCA	GGT	AAT	GAG	2250
E	N	I	F	I	I	D	P	R	S	C	D	I	H	T	N	V	S	M	D	645
GAG	AAT	ATC	TTC	ATA	ATT	GAT	CCA	CGA	TCA	TGT	GAC	ATC	CAT	ACC	AAC	GTT	AGC	ATG	GAT	2310
S	V	P	Y	T	E	W	E	L	S	V	I	I	Q	D	K	G	N	P	Q	665
TCT	GTT	CCC	TAC	ACA	GAA	TGG	GAG	CTG	TCA	GTT	ATC	ATT	CAG	GAC	AAA	GGC	AAT	CCT	CAG	2370
L	H	T	K	V	L	L	K	C	M	I	F	E	Y	A	E	S	V	T	S	685
CTA	CAT	ACC	AAA	GTC	CTT	CTG	AAG	TGC	ATG	ATC	TTT	GAA	TAT	GCA	GAG	TCG	GTG	ACA	AGT	2430
T	A	M	T	S	V	S	Q	A	S	L	D	V	S	M	I	I	I	I	S	705
ACA	GCA	ATG	ACT	TCA	GTA	AGC	CAG	GCA	TCC	TTG	GAT	GTC	TCC	ATG	ATA	ATA	ATT	ATT	TCC	2490
L	G	A	I	C	A	V	L	L	V	I	M	V	L	F	A	T	R	C	N	725
TTA	GGA	GCA	ATT	TGT	GCA	GTG	TTG	CTG	GTT	ATT	ATG	GTG	CTA	TTT	GCA	ACT	AGG	TGT	AAC	2550
R	E	K	K	D	T	R	S	Y	N	C	R	V	A	E	S	T	Y	Q	H	745
CGC	GAG	AAG	AAA	GAC	ACT	AGA	TCC	TAT	AAC	TGC	AGG	GTG	GCC	GAA	TCA	ACT	TAC	CAG	CAC	2610

**Fig. 2E**

H	P	K	R	P	S	R	Q	I	H	K	G	D	I	T	L	V	P	T	I	765
CAC	CCA	AAA	AGG	CCA	TCC	CGG	CAG	ATT	CAC	AAA	GGG	GAC	ATC	ACA	TTG	GTG	CCT	ACC	ATA	2670
N	G	T	L	P	I	R	S	H	H	R	S	S	P	S	S	S	P	T	L	785
AAT	GGC	ACT	CTG	CCC	ATC	AGA	TCT	CAT	CAC	AGA	TCG	TCT	CCA	TCT	TCA	TCT	CCT	ACC	TTA	2730
E	R	G	Q	M	G	S	R	Q	S	H	N	S	H	Q	S	L	N	S	L	805
GAA	AGA	GGG	CAG	ATG	GGC	AGC	CGG	CAG	AGT	CAC	AAC	AGT	CAC	CAG	TCA	CTC	AAC	AGT	TTG	2790
V	T	I	S	S	N	H	V	P	E	N	F	S	L	E	L	T	H	A	T	825
GTG	ACA	ATC	TCA	TCA	AAC	CAC	GTG	CCA	GAG	AAT	TTC	TCA	TTA	GAA	CTC	ACC	CAC	GCC	ACT	2850
P	A	V	E	V	S	Q	L	L	S	M	L	H	Q	G	Q	Y	Q	P		844
CCT	GCT	GTT	GAG	GTC	TCT	CAG	CTT	CTT	TCA	ATG	CTT	CAC	CAG	GGG	CAA	TAT	CAG	CCA		2907
R	P	S	F	R	G	N	K	Y	S	R	S	Y	R	Y	A	L	Q	D	M	864
AGA	CCA	AGT	TTT	CGA	GGA	AAC	AAA	TAT	TCC	AGG	AGC	TAC	AGA	TAT	GCC	CTT	CAA	GAC	ATG	2967
D	K	F	S	L	K	D	S	G	R	G	D	S	E	A	G	D	S	D	Y	884
GAC	AAA	TTT	AGC	TTG	AAA	GAC	AGT	GGC	CGT	GGT	GAC	AGT	GAG	GCA	GGA	GAC	AGT	GAT	TAT	3027
D	L	G	R	D	S	P	I	D	R	L	L	G	E	G	F	S	D	L	F	904
GAT	TTG	GGG	CGA	GAT	TCT	CCA	ATA	GAT	AGG	CTG	CTG	GGT	GAA	GGA	TTC	AGC	GAC	CTG	TTT	3087

**Fig. 2F**

L	T	D	G	R	I	P	A	A	M	R	L	C	T	E	E	C	R	V	L	924	
CTC	ACA	GAT	GGA	AGA	ATT	CCA	GCA	GCT	ATG	AGA	CTC	TGC	ACG	GAG	GAG	TGC	AGG	GTC	CTG	3147	
G	H	S	D	Q	C	W	M	P	P	L	P	S	P	S	S	D	Y	R	S	944	
GGA	CAC	TCT	GAC	CAG	TGC	TGG	ATG	CCA	CCA	CTG	CCC	TCA	CCG	TCT	TCT	GAT	TAT	AGG	AGT	3207	
N	M	F	I	P	G	E	E	F	P	T	Q	P	Q	Q	Q	H	P	H	Q	964	
AAC	ATG	TTC	ATT	CCA	GGG	GAA	GAA	TTC	CCA	ACG	CAA	CCC	CAG	CAG	CAG	CAT	CCA	CAT	CAG	3267	
S	L	E	D	D	A	Q	P	A	D	S	G	E	K	K	K	S	F	S	T	984	
AGT	CTT	GAG	GAT	GAC	GCT	CAG	CCT	GCA	GAT	TCC	GGT	GAA	AAG	AAG	AAG	AGT	TTT	TCC	ACC	3327	
F	G	K	D	S	P	N	D	E	D	T	G	D	T	S	T	S	S	L	L	1004	
TTT	GGA	AAG	GAC	TCC	CCA	AAC	GAT	GAG	GAC	ACT	GGG	GAT	ACC	AGC	ACA	TCA	TCT	CTG	CTC	3387	
S	E	M	S	S	V	F	Q	R	L	L	P	P	S	S	L	D	T	Y	S	E	1024
TCG	GAA	ATG	AGC	AGT	GTG	TTC	CAG	CGT	CTC	TTA	CCG	CCT	TCC	CTG	GAC	ACC	TAT	TCT	GAA	3447	
C	S	E	V	D	R	S	N	S	L	E	R	R	K	G	P	L	P	A	K	1044	
TGC	AGT	GAG	GTG	GAT	CGG	TCC	AAC	TCC	CTG	GAG	CGC	AGG	AAG	GGA	CCC	TTG	CCA	GCC	AAA	3507	
T	V	G	Y	P	Q	G	V	A	A	W	A	A	S	T	H	F	Q	N	P	1064	
ACT	GTG	GGT	TAC	CCA	CAG	GGG	GTA	GCG	GCA	TGG	GCA	GCC	AGT	ACG	CAT	TTT	CAA	AAT	CCC	3567	

**Fig. 2G**

T	T	N	C	G	P	P	L	G	T	H	S	S	V	Q	P	S	S	K	W	1084
ACC	ACC	AAC	TGT	GGG	CCG	CCA	CTT	GGA	ACT	CAC	TCC	AGT	GTG	CAG	CCT	TCT	TCA	AAA	TGG	3627
L	P	A	M	E	E	I	P	E	N	Y	E	E	D	D	F	D	N	V	L	1104
CTG	CCA	GCC	ATG	GAG	GAG	ATC	CCT	GAA	AAT	TAT	GAG	GAA	GAT	GAT	TTT	GAC	AAT	GTG	CTC	3687
N	H	L	N	D	G	K	H	E	L	M	D	A	S	E	L	V	A	E	I	1124
AAC	CAC	CTC	AAT	GAT	GGG	AAA	CAC	GAA	CTC	ATG	GAT	GCC	AGT	GAA	CTG	GTG	GCA	GAG	ATT	3747
N	K	L	L	Q	D	V	R	Q	S	*										1134
AAC	AAA	CTG	CTT	CAA	GAT	GTC	CGC	CAG	AGC	TAG										3780
GAG	ATTTAG	CGAAG	CATTTT	TGTTTCC	ATGTATAT	TGGAAATAG	GGAAACAACAACA	CAAAACCCCTG	AAAGAAC											3859
TGG	CAT	TGCC	AAATAG	TGCA	TTTAT	CATAAA	ATGTG	TCTGTAT	ATTGA	ATATTAA	ATACTGTAT	TTTTCGTAT	GTACA							3938
CAATG	CAAGT	GTGAT	TTTAA	TCTGTAT	TTTAA	AAATACAT	TTGTAC	CTTATAT	TTATGT	GTAAATTTA	ACAACAAA									4017
TTTTAT	TTTTTT	TACTCC	ATGAC	AGACAT	GTGTTT	TCC	TAGTCGT	GTAGAA	AACTAG	CCACTGTT	CAAACTGAT	ACACTA								4096
TTCAAC	CACAAAGT	GTAAAG	CACTGCT	TAGATTAG	TTTGT	TGGGAAG	AAATATTAT	GTGTGAT	GAACAACCC	CACT										4175
GAAG	CATTATACA	ATTCTTA	ATTC	CAATTAAG	TGATCC	CACTTTT	TTC	AACTTTT	TAGAAATTA	AGATCA	TTAAA									4254
ATTGTT	AAGCTATTT	TATTTG	TATTTCT	CACTTCT	ACTAG	CCCCAATAG	TTGA	ACTCTTATAG	GAATA	TCGAA	AGA									4333
TAAAGT	GAAAGTTT	TATTC	AGGACTG	AGAAATAT	CTTGA	AGGTTATTTAT	TAGAT	GACTATCT	CAAAATGA	ACTTTT	TAT									4412
AGACA	ATGATGA	AAACAG	AACTAA	AGTCAATG	TTTCTG	ACTCC	AGCCCC	TACTATTC	CAGGCC	ATCAC	ACTGGCCT									4491
GTCCG	GAGATATTT	CTCTC	ACAATAT	TATATCT	ACTTATA	ATTATG	GTAACA	ATAAATTT	TATTC	ATCCTT	GTA									4570
GTATG	AAACATG	CTCCA	AGGAAATG	GAATCTG	TCCCTTAA	ATGGATA	ACAGTATG	TCTTAATG	GCATAA	ATATAC										4649
TGG	ATAAAAC	AGTTGT	GTGTC	TCTCCT	TAAGT	AGTAAATATA	ATTG	ACTTATTCT	GAAACCC	ATTCTATTT	TGAA									4728

Fig. 2H

TCTCCCCTTTCCCTCTCACAAATACCTTGAACATTTTAAATCCTTTTGGAAATATTGTCCTTTCTTTTGGTTATAAACTATTTCATTTT 4807  
AGCTTTTGTCCTCCAGTGCATGATCTCATATTTTGTGCTTTTATTTTAGTATAAGAACATTTTATATAAAATCATATTTTGT 4886  
TACTGCAATTGTTTATTGTTGTGGCAAAATGAGAAATCCCTTTATTATTGCTGTGATCTCTCTGTGGAATGC 4965  
CTTGGTGAGAGAGATGCTTATTATGACTATTATCATTTCTGACCAAGCTTCTATTAAATGTTATTCTTAATAATACACTA 5044  
TCTTGATTGTACTCTCCAGAAAATTTTCTGTCTCAGTGAAAAATAAAGAAAAATTAAGTAAAAAATAAAAAA 5118

**Fig. 2I**

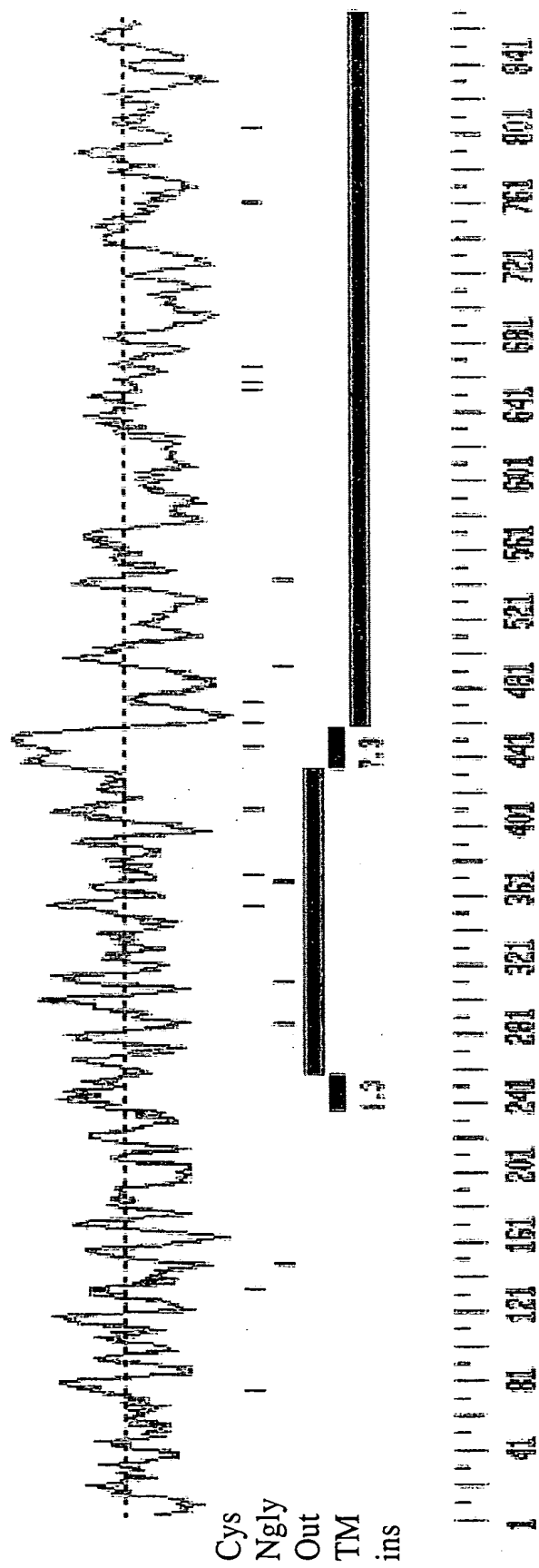


Fig. 3

T416	1651	GAAAAGAGATCTGAGTATAGTTTGGACTGTAATCGCTGAGGACAGGGGGAC	1700
AL137471	1	...AAGAGATCTGAGTATAGTTTGGACTGTAATCGCTGAGGACAGGGGGAC	47
T416	1701	ACCCAGTCTCTTACAGTGAAACATTTTACAGTTCAAATCAATGATATCA	1750
AL137471	48	ACCCAGTCTCTTACAGTGAAACATTTTACAGTTCAAATCAATGATATCA	97
T416	1751	ATGACAATCCACCCCACTTCCAGAGAAAGCCGATATGAATTGTAAATTCA	1800
AL137471	98	ATGACAATCCACCCCACTTCCAGAGAAAGCCGATATGAATTGTAAATTCA	147
T416	1801	GAAAATAACTCACCCAGGGGCATATATCACCACTGTTACAGCCACAGATCC	1850
AL137471	148	GAAAATAACTCACCCAGGGGCATATATCACCACTGTTACAGCCACAGATCC	197
T416	1851	TGATCTTGGAGAAAATGGGCAAGTGACATACACCATCTTGGAGAGTTTA	1900
AL137471	198	TGATCTTGGAGAAAATGGGCAAGTGACATACACCATCTTGGAGAGTTTA	247
T416	1901	TTCTAGGAAGTTCCATAAATACTACATATGTAAACCATTGACCCCATCTAATGGA	1950
AL137471	248	TTCTAGGAAGTTCCATAAATACTACATATGTAAACCATTGACCCCATCTAATGGA	297

FIG. 4A



T416	1951	GCCATCTATGCCCTCAGAAATCTTTGATCATGAAGAAGTGAGTCAGATCAC	2000
AL137471	298	GCCATCTATGCCCTCAGAAATCTTTGATCATGAAGAAGTGAGTCAGATCAC	347
T416	2001	TTTTGTGGTAGAAGCAAGAGATGGAGGAAGCCCCGAAGCAACTGGTAAGCA	2050
AL137471	348	TTTTGTGGTAGAAGCAAGAGATGGAGGAAGCCCCGAAGCAACTGGTAAGCA	397
T416	2051	ATACCACAGTTGTGCTCACCATCATTTGACGAAATGACAACGTTCCCTGTG	2100
AL137471	398	ATACCACAGTTGTGCTCACCATCATTTGACGAAATGACAACGTTCCCTGTG	447
T416	2101	GTTATAGGGCCCTGCATTGCGTAATAATACGGCAGAAATCACCATTCCCAA	2150
AL137471	448	GTTATAGGGCCCTGCATTGCGTAATAATACGGCAGAAATCACCATTCCCAA	497
T416	2151	AGGGGCTGAAAGTGGCTTTCATGTCAACAAGATAAGGGCAATTGACAGAG	2200
AL137471	498	AGGGGCTGAAAGTGGCTTTCATGTCAACAAGATAAGGGCAATTGACAGAG	547
T416	2201	ACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCCATAGTAGCAGGTAATGAG	2250
AL137471	548	ACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCCATAGTAGCAGGTAATGAG	597

FIG. 4B

T416	2251	GAGAAATATCTTCATAAATTGATCCACGATCATGTGACATCCATACCAACGT	2300
AL137471	598	GAGAAATATCTTCATAAATTGATCCACGATCATGTGACATCCATACCAACGT	647
T416	2301	TAGCATGGATTCTGTTCCTTACACAGAAATGGGAGCTGTCAGTTATCATTC	2350
AL137471	648	TAGCATGGATTCTGTTCCTTACACAGAAATGGGAGCTGTCAGTTATCATTC	697
T416	2351	AGGACAAAAGGCAATCCTCAGCTACATACCAAAGTCCTTCTGAAGTGCATG	2400
AL137471	698	AGGACAAAAGGCAATCCTCAGCTACATACCAAAGTCCTTCTGAAGTGCATG	747
T416	2401	ATCTTTGAAATATGCAGAGTCGGTGACAAAGTACAGCAATGACTTCAGTAAG	2450
AL137471	748	ATCTTTGAAATATGCAGAGTCGGTGACAAAGTACAGCAATGACTTCAGTAAG	797
T416	2451	CCAGGCATCCTTGGATGTCCTCCATGATAATAATTATTTCCCTTAGGAGCAA	2500
AL137471	798	CCAGGCATCCTTGGATGTCCTCCATGATAATAATTATTTCCCTTAGGAGCAA	847
T416	2501	TTTGTGCAGTGTGTGCTGGTTATTATGGTGCTATTGTGCAACTAGGTGTAAC	2550
AL137471	848	TTTGTGCAGTGTGTGCTGGTTATTATGGTGCTATTGTGCAACTAGGTGTAAC	897

FIG. 4C

T416	2551	CGCGAGAAAGAAAGACACTAGATCCTATACTGACGGTGGCCGAATCAAC	2600
AL137471	898	CGCGAGAAAGAAAGACACTAGATCCTATACTGACGGTGGCCGAATCAAC	947
T416	2601	TTACCAGCACCCCAAAAAGGCCATCCCGGCAGATTTCACAAAAGGGGACA	2650
AL137471	948	TTACCAGCACCCCAAAAAGGCCATCCCGGCAGATTTCACAAAAGGGGACA	997
T416	2651	TCACATTGGTGCCCTACCATAAATGGCACTCTGCCCATCAGATCTCATCAC	2700
AL137471	998	TCACATTGGTGCCCTACCATAAATGGCACTCTGCCCATCAGATCTCATCAC	1047
T416	2701	AGATCGTCTCCATCTTCAATCTCCTACCTTAGAAAAGAGGGCAGATGGGCAG	2750
AL137471	1048	AGATCGTCTCCATCTTCAATCTCCTACCTTAGAAAAGAGGGCAGATGGGCAG	1097
T416	2751	CCGGCAGAGTCACAACAGTCAACCAGTCACCTCAACAGTTTGGTGACAAATCT	2800
AL137471	1098	CCGGCAGAGTCACAACAGTCAACCAGTCACCTCAACAGTTTGGTGACAAATCT	1147
T416	2801	CATCAAACACGTGCCAGAGAAATTTCTCATTTAGAACTCACCCACGCCACT	2850
AL137471	1148	CATCAAACACGTGCCAGAGAAATTTCTCATTTAGAACTCACCCACGCCACT	1197

FIG. 4D

T416	2851	CCTGCTGTGAGCAGGTCCTCTCAGCTTCTTTCAATGCTTCACCAGGGCA	2900
AL137471	1198	CCTGCTGTGAGCAGGTCCTCTCAGCTTCTTTCAATGCTTCACCAGGGCA	1247
T416	2901	ATATCAGCCAAAGACCAAGTTTTCGAGGAAACAAATATTCCAGGAGCTACA	2950
AL137471	1248	ATATCAGCCAAAGACCAAGTTTTCGAGGAAACAAATATTCCAGGAGCTACA	1297
T416	2951	GATATGCCCTTCAAGACATGGACAAATTTAGCTTGAAAGACAGTGGCCGT	3000
AL137471	1298	GATATGCCCTTCAAGACATGGACAAATTTAGCTTGAAAGACAGTGGCCGT	1347
T416	3001	GGTGACAGTGAGGCAGGAGACAGTGATTATGATTGGGGCCGAGATTCTCC	3050
AL137471	1348	GGTGACAGTGAGGCAGGAGACAGTGATTATGATTGGGGCCGAGATTCTCC	1397
T416	3051	AATAGATAGGCTGCTGGGTGAAGGATTCAGCGACCTGTTTCTCACAGATG	3100
AL137471	1398	AATAGATAGGCTGTTGGGTGAAGGATTCAGCGACCTGTTTCTCACAGATG	1447
T416	3101	GAAGAAATTCAGCAGCTATGAGACTCTGCACGGAGGAGTGCAGGGTCCCTG	3150
AL137471	1448	GAAGAAATTCAGCAGCTATGAGACTCTGCACGGAGGAGTGCAGGGTCCCTG	1497

FIG. 4E

T416	3151	GGACACTCTGACCAGTCTGGATGCCACCACTGCCCTCACCGTCTTCTGA	3200
AL137471	1498	GGACACTCTGACCAGTCTGGATGCCACCACTGCCCTCACCGTCTTCTGA	1547
T416	3201	TTATAGGAGTAACATGTTTCATTCCAGGGGAAGAAATTCCCAACGCAACCCC	3250
AL137471	1548	TTATAGGAGTAACATGTTTCATTCCAGGGGAAGAAATTCCCAACGCAACCCC	1597
T416	3251	AGCAGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT	3300
AL137471	1598	AGCAGCAGCATCCACATCAGAGTCTTGAGGATGACGCTCAGCCTGCAGAT	1647
T416	3301	TCCGGTGAAAAGAAAGAGTTTTTTCCACCTTTTGGAAGGACTCCCCAAA	3350
AL137471	1648	TCCGGTGAAAAGAAAGAGTTTTTTCCACCTTTTGGAAGGACTCCCCAAA	1697
T416	3351	CGATGAGGACACTGGGGATACCAGCACATCATCTCTGCTCTCGGAAATGA	3400
AL137471	1698	CGATGAGGACACTGGGGATACCAGCACATCATCTCTGCTCTCGGAAATGA	1747
T416	3401	GCAGTGTGTTCCAGCGTCTCTTACCGCCCTTCCCTGGACACCTATTCTGAA	3450
AL137471	1748	GCAGTGTGTTCCAGCGTCTCTTACCGCCCTTCCCTGGACACCTATTCTGAA	1797

FIG. 4F

T416	3451	TGCAGTGAGGTGGATCGGTCCAACTCCCTGGAGCGCAGGAAGGACCCTT	3500
AL137471	1798	TGCAGTGAGGTGGATCGGTCCAACTCCCTGGAGCGCAGGAAGGACCCTT	1847
T416	3501	GCCAGCCAAAACACTGTGGGTTACCCACAGGGGGTAGCGGCATGGGCAGCCA	3550
AL137471	1848	GCCAGCCAAAACACTGTGGGTTACCCACAGGGGGTAGCGGCATGGGCAGCCA	1897
T416	3551	GTACGCAATTTTCAAAATCCCACCACCAACTGTGGCCGCCACTTGGAAC	3600
AL137471	1898	GTACGCAATTTTCAAAATCCCACCACCAACTGTGGCCGCCACTTGGAAC	1947
T416	3601	CACGCCAGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGAT	3650
AL137471	1948	CACGCCAGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGAT	1997
T416	3651	CCCTGAAAATTATGAGGAAGATGATTTTGACAAATGTGCTCAACCACCTCA	3700
AL137471	1998	CCCTGAAAATTATGAGGAAGATGATTTTGACAAATGTGCTCAACCACCTCA	2047
T416	3701	ATGATGGGAAACACGAACTCATGGATGCCAGTGAAC	3750
AL137471	2048	ATGATGGGAAACACGAACTCATGGATGCCAGTGAAC	2097

FIG. 4G

T416	3751	AACA	AACTGCTTCAAGATGTCCGCCAGAGCTAGGAGATTTTAGCGAAGCA	3800
AL137471	2098	AACA	AACTGCTTCAAGATGTCCGCCAGAGCTAGGAGATTTTAGCGAAGCA	2147
T416	3801	TTTT	TGTTCCATGTATATGGAAATAGGGAACAACAACAACAAAAA	3850
AL137471	2148	TTTT	TGTTCCATGTATATGGAAATAGGGAACAACAACAACAAAAA	2197
T416	3851	CCCT	GAAAGAACTGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTC	3900
AL137471	2198	CCCT	GAAAGAACTGGCATTGCCAAATAGTTGCATTTATCATAAATGTGTC	2247
T416	3901	TGTG	TATATTGAATATTAAATACTGTATTTTCGTATGTACACAAATGCAAG	3950
AL137471	2248	TGTG	TATATTGAATATTAAATACTGTATTTTCGTATGTACACACAAAAAA	2297
T416	3951	TGTG	ATTATTTTAAATCTGTATTTTAAATAACATTTGTACCTTATATTTA	4000
AL137471	2298	AAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG.....	2338

FIG. 4H

T416	1	...	ATGCACCAAATG..AATGCTAAAAATGCAC	TTTAGGTTTGT	TTT	TGCA	45
m-PC	1	ATGATGCTACTTCTG	CCCATTCCTGCTAGGGCTCTTAGGGCCAGGAAGCTA				50
T416	46	CTTCTGATAGTATCTTTCA	ACCACGATGTA	CTGGCA...	AGAATTTGAA		92
m-PC	51	CT..TGTTCA	TTTCAGGGGATTGT	CAGGAGGTGGCCACTGT	TCATGGTGAA		98
T416	93	ATACAGGATTTATGAGGA	ACAGAGGGTTGGATCAGTA	ATTGCAAGACTAT			142
m-PC	99	ATTCCAAAGTGACAGAGGA	AGTGCCGCTCTGGCACGGTGATAGGGA	AACTGT			148
T416	143	CAGAGGATGTGGCTGATGTTT	TATTGAAGCTTCCTAATCCTTCTACTGTT				192
m-PC	149	CCCAAGAACT..AGA.GTGGAGGAGAGGCGTG	GGGAAGGCAGGAGATG..				193
T416	193	CGATTT	CGAGCCATGCAGAGGGGAAATTCTCCTCTACTTGTAGTAAACGA				242
m-PC	194	CCTTCCAGATT	CTGCAGCTGCCCTCAGGCACTGCCCGTT	CAGATGA	ACTC		242

FIG. 5A



T416	243	GGATAATGGGAAATCAGCATAGGGCTACAATTGACCGTGAACAAC	292
m-PC	243	TGAGACGGCCTGCTCAGCACTTCCAGCCGGCTGGATCGGAGAAGCTAT	292
T416	293	GCCAGAAAACTTGAACCTGTTCATAGAGTTTGATGTGATCACTCTACCC	342
m-PC	293	GTCGGCAGGAAGATCCCCTGTCTGTGTCTCATTTGACGTG.....CTTGCC	336
T416	343	ACA.GAGCATCTGCAGCTTTTCCATATTTGAAGTTGAAGTGCTGGATATTA	391
m-PC	337	ACAGGGCGTCTGC.TCTAATTCAATGTGGAGATTCAGGTGCTAGACATCA	385
T416	392	ATGACAAATCTCCCCAGTTTTCAGATCTCTCATACCTATTGAGATATCT	441
m-PC	386	ATGACCACCCAGCCACAGTTTCCCCAAAGACGACGAGGAATGGAAATCTCA	435
T416	442	GAGAGTGCAGCAGTTGGGACTCGCATTTCCCCTGGACACAGTGCAATTTGATCC	491
m-PC	436	GAGAGTGCCTCTCTGCACACACGAATCCCCCTTGGACACAGAGCTCTTGACCA	485

FIG. 5B

T416	492	AGATGTTGGGAAAAATTCCCTCCACACATACTCGCTCTCTGCCAATGATT	541
m-PC	486	AGACACGGGTCCTAACAGCTTATATTCCTACTCCCTGTCTCTCCAGTGAAC	535
T416	542	TTTTTAATATCGAGGTTTCGGACCAGGACTGATGGAGCCAAGTATGCAGAA	591
m-PC	536	ACTTTGCCCTGGATGTTATTGTGGCCCTGATGAGACCAACATGCAGAG	585
T416	592	CTCATAGTGGTCAGAGAGTTAGATCGGGAGCTGAAGTCAAGCTACGAGCT	641
m-PC	586	CTTGTTGGTGAAGGAGTTGGACAGGGAACCTCCACTCATATTTTGATCT	635
T416	642	TCAGCTCACTGCCCTCAGAC.ATGGGAGTACCTCAGAGGTCCTGGCTCATCC	690
m-PC	636	GGTGCTGACCGCCTATGACAAATGGGAAT.CCCCCTAAGTCAGGAATCAGC	684
T416	691	ATACTAAAAATAAGCATTTTCAGACTCCAATGACAACAGCCCTGCTTTTGA	740
m-PC	685	GTGGTCAAGGTCAATGTCTCTGGACTCCAATGACAATAAGTCCAGTGTTCGC	734

**FIG. 5C**

T416	741	GCAGCAATCTTATATAATAACAACCTCTTAGAAAACTCCCCGGTTGGCACTT	790
m-PC	735	TGAGAGTTCACTAGCACTAGAAAATCCCAGAAAGACACACTGTTCCCTGGTACTC	784
T416	791	TGCTCTTAGATCTGAATGCCACGGATCCAGATGAGGGCGCTAATGGGAAA	840
m-PC	785	TTCTCATAAACCTGACTGCTACAGATCCCCGACCAAGGACCCAATGGGGAG	834
T416	841	ATTGTATATTCCCTTCAGCAGTCATGTGTCTCCCCAAAAATTATGGAGACTTT	890
m-PC	835	GTAGAGTTCTTCTTTGGCAAGCATGTGTCTCCCCAGAGGTGATGAACACCTT	884
T416	891	TAAAAATTGATTCTGAAAAGAGGACATTTGACTCTTTTCAAGCAAGTGGATT	940
m-PC	885	TGGCATAGATGCCAAGACAGCGCCAGATCATTTCTGCGCCAAGCCCTAGATT	934
T416	941	ATGAAATCACCCAAATCCCTATGAGATTGATGTTCAAGGCTCAAGATTGGGT	990
m-PC	935	ACGAGAAGAACCCTGCCTATGAGGTGGATGTCCAGGCAAGGGATTGGGT	984

**FIG. 5D**



T416	1238	ACAATTATTTAACTTAACTAATGCCACACTGGATAGAGAAAAGAGATCT	1287
m-PC	1223	ACACGTACATGCTGCTCACCCAATGCCACACTGGACACAGAGCAGTGGCCC	1272
T416	1288	GAGTATAGTTTGACTGTAAATCGCTGAGGACAGGGGGACACCCAGTC..TC	1335
m-PC	1273	ATATATACTCTCACTGTGTTTGCCCAAGAC.CAAGGAC.CCCAGCCCTTA	1320
T416	1336	TCTACAGTGAAACATTTTACAGTTCAAATCAATGATATCAATGACAATCC	1385
m-PC	1321	TCAGCTGAGAAGGAGCTCCAAATTCAGGTTAGTGATGTCAATGACAATGC	1370
T416	1386	ACCCCACTTCCAGAGAAGCCGATATGAATTTGTAATTCAGAAAATAACT	1435
m-PC	1371	CCCTGTGTTTGAGAGAAGCCGGTACGAGGTCCTCCACTTGGGAAAATAACC	1420
T416	1436	CACCAGGGGCATATATCACCACCTGTTACAGCCACAGATCCTGATCTTGA	1485
m-PC	1421	CACCCCTCTCTTCACCTCATCAGCTCAAAGCGCATGATGCTGACTTGGGC	1470

**FIG. 5F**

T416	1486	GAAAATGGGCAAGTGACATACACCATCTTGA.GAGTTTATTCT.AGGA	1533
m-PC	1471	AGTAATGGAAAAGTGTCATACCGTATCAAGGACTCCCCCGTTTCTCACTT	1520
T416	1534	AGTTCCATAACTACATATGTAACCATTGA...CCCATCTAATGGAGCCAT	1580
m-PC	1521	AGT..CATTATTGACTTTGAAACAGGAGAAGTCACTGCTCAGAGGTCACT	1568
T416	1581	...CTATGCCC...TCAGAAATCTTTGA..TC...ATGA.AGAAGTGAGTC	1618
m-PC	1569	GGACTATGAACACAGATGGCAGGCTTTGAGTTCAGGTGATAGCAGAG.GAC	1617
T416	1619	AGATCAC.TTTTGTGGTAGAAGCAAGAGATGGAGGAAGCCCGAAGCAACT	1667
m-PC	1618	AGAGGGCAACCCAGCTCGCATCCAG.CATCTCGGTGTGGGTAGCCTCT	1666
T416	1668	GGTAAGC.....AATACCACAGTTGTG.CTCACC.....ATCATTGAC	1704
m-PC	1667	TGGATGCCAATGATAATGCCCCAGAAAGTGATTACGCCCTGTGCTCAGTGAA	1716

**FIG. 5G**

T416	1705	GAAAATGACAACGTTCTGTGGTTATA.....GGGCC.....	1736
m-PC	1717	GGCAAAGCCACCCCTTTCGGTGCTTGTAATGCCTCCACGGCCACCTTCT	1766
T416	1737	..TG..CATTGCGTA.....AT.AATACGGCAGAAATCACCATTCT	1771
m-PC	1767	GTTGCCCATTTGAGAATCCAGTGGCATGGATCCAGCAGGTACTGGTATAC	1816
T416	1772	..CCAAAGG.GGCTGAAAG....TGG.CTTT.CATGTCACAAGAATAAGG	1812
m-PC	1817	CACCAAAGGCTACCCACAGCCCCCTGGTCTTTCCCTTTTGTTAACAATCGTG	1866
T416	1813	GCAATTGACAGAGACTCTGGTGTGAATGCTGAACCTCAGCTGCGCCATAGT	1862
m-PC	1867	GCTAGGGAATGCAGACTCGGGGGCCCAATGGGGAACCTCTTCTACAGCATTCA	1916
T416	1863	AGCAGGTAATGAGGAGAAATATCTTCATAAATTGATCCACGATCATGTGACA	1912
m-PC	1917	AAGTGGGAATGATGCTCATCTCTT.TTTCCTCAGCC.CTTCCCTTGGGGCA	1964

FIG. 5H

T416	1913	TCCAT..ACCAACGTTAGC.ATGGATTCTGTTCCTTCCCTACACAG..AATGGG	1957
m-PC	1965	GCTATTCAATTAATGTCACCAATGCCAGCAGCCTCATCGGGAGTCAGTGGG	2014
T416	1958	AGCTGTCAAGTTATCATTCAGGACAAAGGCAATCCTCAGCTACATACCAA	2007
m-PC	2015	ACCTGGGGATAGTGGTAGAGGACCAGGGCAGCCCCCTCCTTGCAGACCCAA	2064
T416	2008	GTCCCTTCTGAAGTGCATGATCTTTGAATATGCAGAGTCGGTGACAAGTAC	2057
m-PC	2065	GTTTCATTGAAGGTCGTG...TTTG..TCACCAGTGT..GGACCACCTAA	2107
T416	2058	AGCAATGACTTCAGTAAGCCAGGCATCCTTGGATGTCTCCATGA.TAATA	2106
m-PC	2108	GGGATTCTGCTCA.TGAGCCCGGAGTTCT..GAGCACACCAGCAGCTGGCT	2154
T416	2107	ATTATTTCCCTTAGGAGCAATTGTGTCAGTGTTCGCTGGTTATTATGGTGCT	2156
m-PC	2155	TTGATCTGCCCTGGCTGTACTGCTGGCCATCTTTGGATTGCTCTTAGCCCT	2204

**FIG. 5I**



T416	2157	ATTGCAACTAGGTGTAACCGGAGAAAGACACTAGATCCTATAACT	2206
m-PC	2205	GTTCGTGTCCATCTGCAGGACAGAGAGAAAGGATAATAGGGCCTACAAC	2254
T416	2207	GCAGGGTGGCCGAATCAACTTACCAGCACCCCAAAAGGCCATCCCGG	2256
m-PC	2255	GTCGAGAAGCTGAGTCGTCAATACCGCCACCAGCCCAAGAGGCCCCAGAAA	2304
T416	2257	CAGATTCACAAAGGGGACATCACATTGGTGCCCTACCATAAATGGCACTCT	2306
m-PC	2305	CACATTCAAGAAGGCAGATATCCACCTGGTGCCCTGTGCT.TAGGGCCAC.	2352
T416	2307	GCCCATCAGATCTCATCA...CAGATCGTCTC.CATCTTCATCTCCTA..	2350
m-PC	2353	GAGAATGAGA.CTGATGAAGTCAGGCCATCTCACAAAGGATACCAGCAAGG	2401
T416	2351	..CCTTAGAAAGAGGGCAGATGGG.....CAGCCGGCAGAGTCACAA	2390
m-PC	2402	AGACACTGATGGAGGCAGGCTGGGACTCTTGCCCTGGAGGCCCCCTTCCAC	2451

FIG. 5J

T416	2391	CAGTCACCAGTCACTCAACAGTTTGGTGACAAATCTCATCAAACCACG...	2437
m-PC	2452	CTCACACCA.ACCCTATACAGGACCCTGCGTAACCAAGGCAACCAGGGAG	2500
T416	2438	...TGCCAGA.....GAATTCT.CATTAGAAC.TCACC...CACGCC	2472
m-PC	2501	AACGGCAGAGAGCCAGGAGGTACTGCAGGACACCTTCAACTTCTCTTT	2550
T416	2473	ACTCCTGC..TGTTGA.GCAGGTCTCTC...AGCTTCT...TTCAATGC	2512
m-PC	2551	AACCATCCAGGCAGAGAGGAATGCCTCCCGGAGAACCTAAACCTTCCTGA	2600
T416	2513	TTCAACCAGGGCAATA..TCAGCCAAGACCAAG..TTTTCGAGGAAACAA	2558
m-PC	2601	GTCCCCACCTGCTGTACGCCAACCACTCTTAAGGCCCTCTGAAGGTGCCCTG	2650
T416	2559	ATATTCCAGGAGCTACAGATA.TGCCCTTCAAGACATGGACAAATTAGC	2607
m-PC	2651	GTAGCCCCATAGCGAGGGCGACTGGAGACCAAGACAAGGAGGA...GGC	2696

FIG. 5K

T416	2608	TTGAAAGACAGTGGCCGTGGTGACAGTGAGGC..AGGAGACAG.TGATTAT	2654
m-PC	2697	CCCACAGAGCCCCACCAGCGTCCCTCTGCAACCCCTAAGACGACACAGCGGAATT	2746
T416	2655	TGATTTGGGGCGAGATTCTCCAATA.GATAGGCTGCTGGGTGAAGGATTC	2703'
m-PC	2747	TCAAT..GGCAAAGTGTCTCCTAGAGGAGAGTCCGGTCCCTCATCAGATTC	2794
T416	2704	..AGCGACCTGTTT...CTCACAGATGGAAGAATTCCAGCAGCTATGAGA	2748
m-PC	2795	TGAGGAGCCTGGTTAGGCTCTCTG.TGGCTGCTTTTGCGGA...ACGGAA	2840
T416	2749	CTCTGCACGGAGGAG..TGCAGGGTCCTGGGACACTCTGACCAGTGCTGG	2796
m-PC	2841	CCCGG..TGGAGGAGCCTGCTGGGACT..CTCCTCCTGTCCAGCAAATC	2886
T416	2797	ATGCCACCACCTGCCCTCAC...CGTCTTCTGATTATAGGAGTAACATGT	2842
m-PC	2887	TCCCAGCTGCTGCTCCTTGCTGCACCCAGGGCCAATTCCAGCCCAACCAAA	2936

**FIG. 5L**

T416	2843	TCATTCCAGGGGAAGAATTCCCAACGCAACCCAGCAGCAGCATC.....	2887
m-PC	2937	CCA..CCGAGGAAATAAATACTTGGCCAAGCCCCGGCGCAGCAGCAGGGG	2984
T416	2888	.CACATCAGAGTC.TTGAGGATGACGCTCAGCCTGCAGATTCCGGTGAAA	2935
m-PC	2985	TACCATCCCAGACACAGAGGGCCTTG.TAGGCCCTCAAGCCT.AGTGGCCA	3032
T416	2936	AGAAGAAGAGTTTTTCCACCTTTTGGAAGGACTCCCCAAACGATGAGGAC	2985
m-PC	3033	AGCAGAA.....CCTGACCCTGGAAGAAGGGC.CCCCGAGCCCGGAGGA.	3074
T416	2986	ACTGGGGATACCAGCACATC.ATCTCTGCTCTCGGAAATGAGCAGTGTTGT	3034
m-PC	3075	...GGACCTTTCTGTAAAGCGACTTCTAGAAGAAGAGCTGTCGAGCCTGT	3121
T416	3035	TCCAGCGTCTCTTACCGCCTTCCCTGGACA..CCTATTCTGAATGCAGTG	3082
m-PC	3122	TGGACCCCTAATACAGGTCTAGCCCTGGACAAGCTGAGTCCGCCTGACCCA	3171

**FIG. 5M**

T416	3083	AGGTGGATCG.GTCCAACTCCCTGGAGCGCAGGAAGGACCCTTGCCAGC	3131
m-PC	3172	GCCTGGATGGCGAGATTGTTCATTGCCCCCTCA.....CCACCAATTATCGA	3216
T416	3132	CAAAACTGTGGGTTACCCACAGGGGGTAGCGGCATGGGCAGCCAGTACGC	3181
m-PC	3217	GACAACT.TGTCTTCCCCCGATGCTACAACATCAGAGGAACCGAGAAC..	3263
T416	3182	ATTTTCAAAATCCCACCACTGTGGGCGCCACTTGGAACCTCACTCC	3231
m-PC	3264	.CTTCCAGACATTCCGGCAAGACAGTTGGACCCGGGAC.CCGAGCTGAGCCC	3311
T416	3232	AGTGTGCAGCCTTCTTCAAAATGGCTGCCAGCCATGGAGGAGATCCCT..	3279
m-PC	3312	AACAGGCACGCGCCTGGCCAGCACTTTCGTCTCGGAGATGAGCTCTCTGC	3361
T416	3280	..GAAA..ATTATGAGGAAGATGATTTTGACAATG..TGCT.CAACCACC	3322
m-PC	3362	TGGAATGTGTGTGGGCGACACACGGTACCAGTGGAAGCTGCGTCCGCG	3411

**FIG. 5N**

T416	3323	TCAATGATGGGAAACACGAAC	CTCATGGATG	....	CCAGT	...GA	.....	3359
m-PC	3412	GCTTTGCGGAGGCTCTCGGTGTGCGGGAGGACCCCTCAGTCTAGACCTAGC	3461					
T416	3360	....ACTGGTGGCAGAGATTAA	CAA..ACTGCTT	..CAAGATGTCCGC	.C	3400		
m-PC	3462	CACCAAGTGGGGCTTCAGCTTCAGAAAGCACAGGGTAGAAAGAGGCAGCTG	3511					
T416	3401	AGAGC	.....	3405				
m-PC	3512	AGAGCAGACTTGGCTGTGGCAGGAATCTA	3540					

FIG. 50

m-PC	1	MMLLLPFLGLLPGSYLFISGDCQEVATVMVKFQVTEEVPSGTVIGKLS	50
T416	1	MHQMNAKMHFRVFALLIVSFN.HDVLGKNLKYRIYEEQRVGSVIARLS	48
m-PC	51	QELR..VEERRGKAGDAFQILQLPQALPVQMNSEDGLLSTSSRLDREKLC	98
T416	49	EDVADVLLKLPNPSTVFRFRAMQRGNSPLLVVNEDNGEISIGATIDREQLC	98
m-PC	99	RQEDPCLVSFDV..LATGASALIHVEIQVLDINDHQPFQPKDEQELEISE	146
T416	99	QKNLNCSEFFDVITLPTTEHLQLFHIEVEVLDINDNSPQFSRSLPIEISE	148
m-PC	147	SASLHTRIPLDRALDQDTGPNLSLYSLSLSPSEHFALDVIVGPDETHAEEL	196
T416	149	SAAVGTRIPLDSAFDPDVGENSLHTYSLSANDFFNIEVTRTRTDGAKYAEEL	198
m-PC	197	VVVKELDRELHSHYFDLVLTAYDNGNPPKSGISVVKVNVLDNSNDNSPVFAE	246
T416	199	IVVRELDRELKSSYELQLTASDMGVFQSRGSSILKISISDSNDNSPAFEQ	248

FIG. 6A

m-PC	247	SSLALEIPEDTVPGTLLINLTATDPDQGPNGEVEFFFGKHVSPVMTTFG	296
		: : :   . .         :         :         :	
T416	249	QSYIIQLLENSPVGTLTLLDLNATDPDEGANGKIVYSFSSHVSPKIMETFK	298
m-PC	297	IDAKTGQIILRQALDYEKNPAYEVDVQARDLGPNSIPGHCKVLIKVLDVN	346
		. .   :   . .         .                     : :	
T416	299	IDSERGHLTLFKQVDYEITKSYEIDVQAQDLGPNSIPAHCKIIIKVVDVN	348
m-PC	347	DNAPSILITWAS...QTSLVSEDLPRDSFIALVSANDLDSGNNGLVHCW	392
		:   :   :   :   :   :   :   :   :	
T416	349	DNKPEININLMSPGKEEISYIFEGDPIDTFVALVRVQDKDSGLNGEIVCK	398
m-PC	393	LNQELGHFRLKRTNGNTYMLLTNATLDREQWPIYTLTVFAQDQGPQLSA	442
		.       :   :     :             .   .       :   :	
T416	399	LHGH.GHFKLQKTYENNYLILTNAATLDREKRSEYSLTVIAEDRGTPSLST	447
m-PC	443	EKELQIQVSDVNDNAPVFEEKSRYEVSSTWENNPPSLHLITLKAHDADLGSN	492
		: : :   :       :   :         : :   :	
T416	448	VKHFTVQINDINDNPPHFQRSRYEFVISENNSPGAYITTVTATDPPDLGEN	497

FIG. 6B



m-PC	493	GKVSRIKD.....SPVSHLVIIDFETGETAQRSLDYEQMAGFEFQVIA	537
		. . . .: : . . .: : . . .: : . .	
T416	498	GQVTTYILESFILGSSITTYVTIDPSNGAIYALRIFDHEEVSQITFVVEA	547
		. . . .: : . . .: : . . .: : . .	
m-PC	538	EDRGQP.QLASSISVWVSLLDANDNAPEVIQPVLSEGKATLSVLVNASTG	586
		. . . .: : . . . . . .: : . .	
T416	548	RDGGSPKQLVSNTTVVLTIIDENDNVVVGIPALRNNTAEITIPKGAESG	597
		. . . .: : . . . . . .: : . .	
m-PC	587	HLLLPENPSGMDPAGTGIPPKATHSPWSFLLLTIVARDADSGANGELFY	636
		. . . .: : . . . . . .: : . .	
T416	598	.....FHVTRIRAIDRDSGVNAELSC	618
		. . . .: : . . . . . .: : . .	
m-PC	637	SIQSGNDAHLFFLSPSLGQLFINVTNASSLIGSQWDLGIVVEDQGSPSLQ	686
		. . . .: : . . . . . .: : . .	
T416	619	AIVAGNEENIFIIDPRSCDIHTNV.SMDSVPYTEWELSVIIQDKGNPQLH	667
		. . . .: : . . . . . .: : . .	
m-PC	687	TQVSLKV...FVTSVDHLRDSAHEPGVLSTPALALICLAVLLAIFGLLL	733
		. . . .: : . . . . . .: : . .	
T416	668	TKVLLKCMIFEYAESVTSTAMTSVVSQASLDVSMIIISLGAICAVLLVIM	717
		. . . .: : . . . . . .: : . .	

FIG. 6C

m-PC	734	ALFVSI	CRTER	KNRAY	NCREAE	SSYRHQ	PKRPQ	KHIQ	KADI	HLVP	VLRA	783					
T416	718	VLFAT	RNREK	KDTR	SYNCR	VAESTY	QHHP	KRPS	RQIH	KGDIT	LVPTING	767					
m-PC	784	HENET	DEV	..PSH	KDTS	KETL	MEAG	WDSC	LEAP	FHLT	PTLY	RTL	RN	QGN	831		
T416	768	TLPI	RSHR	SSP	SSPT	LERG	QMGS	RQSH	NSHQ	SLNS	LVTI	SSNH	VPEN	F	817		
m-PC	832	QGE	LAES	QEV	LQD	TFN	FLFN	HPRQ	RNAS	REN	LNLP	ESPP	AVRQ	PLL	RPLK	881	
T416	818	SLE	LTHAT	PAVE	QVSQ	LLSML	HQGQ	YQPR	PSFR	GNKY	SRSY	RYAL	QDM	DK		867	
m-PC	882	VPG	SPIA	RATG	DDKE	EA	PQSP	PASS	ATL	RRQR	NFN	GKV	SPR	GESG	PHQI	931	
T416	868	FS...	LKD	SGRG	DSEAG	SDYD	LG	RDSP	IDR	LLGE	GFSD	FLTD	GRIP	A		913	
m-PC	932	LR	SLV	RLS	VAA	FAER	NPVE	EPAG	DSPP	VQQI	SQ	LLS	LLH	QGQ	FQPK	PNHR	981
T416	914	AM	RLCT	EEC	RVLG	HS	DQC	WMP	PLP	SPSS	DYRS	NMFIP	GEE	FPTQ	PQQQ	HP	963

FIG. 6D

m-PC	982	GNKYLAKPGSSRG	TIPDTEGLVGL.KPSGQAE	PDLEE	GGPPSPEEDLSVK	1030
T416	964	HQLEDDAQPADS	GEKKSFSTFGK	DSPNDEDTG	DTSTSSLLSEMSSVFQ	1013
m-PC	1031	RLLEEEL...	SSLDPNTGLALDKLSP	PDPAWMARLSL	PLTTNYRDNLS	1077
T416	1014	RLPPSLD	TYSECSEVDRSNS	LERRKGPLPAK	TVGYPQGVAAWA	1063
m-PC	1078	PDAT	TSEEPRTFQTFGKT	VGPGPELSPTG	TRLASTFVSEMSSL	1127
T416	1064	NPTNCGPPLG	THS...SVQPSS	KWLPAMEEIPEN	YEEDDFDNV	1110
m-PC	1128	HTVPVEA	AASALRRRLSV	CGRTL	SLDLATSGASASEAQ	1180
T416	1111	GKHE	MDASELVAEIN	KLLQDVRQS	.....	1135

**FIG. 6E**

GAAGTGGGAT	GTGCAAAAGC	GCCGGCTGGA	AATCCCGGCT	GTGTCTCCGT	CAACTCTTTA	60
CGCAACAGAG	GTCTCCCCCT	GCCCTTGTT	TCTACCGGC	CGCCTGCTCC	CACTCGGCGA	120
AAAAAATTAC	ACAACAGCAG	CCGCGGCG	ATG ACG	TGG AGG	GCT GCC TCC	172
	Met Thr	Trp Arg	Ala Ala	Ala Ser		8
ACG TGC	GCG GCG	CTC CTG	ATT CTG	TGG GCG	CTG ACG ACC	GAA GGT 220
Thr Cys	Ala Ala	Leu Leu	Ile Leu	Leu Trp	Ala Leu Thr	Glu Gly 24
GAT CTG	AAA GTA	GAG ATG	ATG GCA	GGG ACT	CAG ATC ACA	CCC CTG 268
Asp Leu	Lys Val	Glu Met	Met Ala	Gly Gly	Thr Gln Ile	Thr Pro Leu 40
AAT GAC	AAT GTC	ACC ATA	TTC TGC	AAT ATC	TTT TAT	TCC CAA CCC CTC 316
Asn Asp	Asn Val	Thr Thr	Ile Phe	Cys Asn	Ile Phe Tyr	Ser Gln Pro Leu 56
AAC ATC	ACG TCT	ATG GGT	ATC ACC	TGG TTT	TGG AAG	AGT CTG ACG TTT 364
Asn Ile	Thr Thr	Ser Met	Gly Ile	Thr Thr	Trp Phe	Lys Ser Leu Thr Phe 72
GAC AAA	GAA GTC	AAA GTC	TTT GAA	TTT TTT	GGA GAT	CAC CAA GAG GCA 412
Asp Lys	Glu Val	Val Lys	Val Phe	Glu Phe	Gly Asp	His Gln Glu Ala 88
TTC CGA	CCT GGA	GCC ATT	GTG TCT	CCA TGG	AGG CTG	AAG AGT GGG GAC 460
Phe Arg	Pro Gly	Ala Ala	Ile Val	Ser Pro	Trp Arg	Leu Lys Ser Gly Asp 104
GCC TCA	CTG CGG	CTG CCT	GGA ATC	CAG CTG	GAG GAA	GCA GGA GAG TAC 508
Ala Ser	Leu Arg	Leu Pro	Gly Ile	Gln Leu	Glu Glu	Ala Gly Glu Tyr 120

**Fig. 7A**

CGA TGT GAG GTG GTG GTC ACC CCT CTG AAG GCA CAG GGA ACA GTC CAG	556
Arg Cys Glu Val Val Val Thr Pro Leu Lys Ala Gln Gly Thr Val Gln	136
CTT GAA GTT GTG GCT TCC CCA GCC AGC AGA TTG TTG CTG GAT CAA GTG	604
Leu Glu Val Val Ala Ser Pro Ala Ser Arg Leu Leu Leu Asp Gln Val	152
GGC ATG AAA GAG AAT GAA GAC AAA TAT ATG TGT GAG TCA AGT GGG TTC	652
Gly Met Lys Glu Asn Glu Asp Lys Tyr Met Cys Glu Ser Ser Gly Phe	168
TAC CCA GAG GCT ATT AAT ATA ACA TGG GAG AAG CAG ACC CAG AAG TTT	700
Tyr Pro Glu Ala Ile Asn Ile Thr Trp Glu Lys Gln Thr Gln Lys Phe	184
CCC CAT CCC ATA GAG ATT TCT GAG GAT GTC ATC ACT GGT CCC ACC ATC	748
Pro His Pro Ile Glu Ile Ser Glu Asp Val Ile Thr Gly Pro Thr Ile	200
AAG AAT ATG GAT GGC ACA TTT AAT GTC ACT AGC TGC TTG AAG CTG AAC	796
Lys Asn Met Asp Gly Thr Phe Asn Val Thr Ser Cys Leu Lys Leu Asn	216
TCC TCT CAG GAA GAC CCT GGG ACT GTC TAC CAG TGT GTG GTA CGG CAT	844
Ser Ser Gln Glu Asp Pro Gly Thr Val Tyr Gln Cys Val Val Arg His	232
GCG TCC TTG CAT ACC CCC TTG AGG AGC AAC TTT ACC CTG ACT GCT GCT	892
Ala Ser Leu His Thr Pro Leu Arg Ser Asn Phe Thr Leu Thr Ala Ala	248
CGG CAC AGT CTT TCT GAA ACT GAG AAG ACA GAT AAT TTT TCC ATT CAT	940
Arg His Ser Leu Ser Glu Thr Glu Lys Thr Asp Asn Phe Ser Ile His	264

**Fig. 7B**

TGG TGG CCT ATT TCA TTC ATT GGT GTT GGA CTG GTT TTA ATT GTT	988
Trp Trp Pro Ile Ser Phe Ile Gly Val Gly Leu Val Leu Ile Val	280
TTG ATT CCT TGG AAA AAG GTA AGG GGC TCC AAA GCA AAG TTC AGC CCT	1036
Leu Ile Pro Trp Lys Lys Val Arg Gly Ser Lys Ala Lys Phe Ser Pro	296
GTG TCT TGG GCT AGT AAA AAG CTT TTA GAG CAG CTG CTG CCA ACC TTA	1084
Val Ser Trp Ala Ser Lys Lys Leu Leu Glu Gln Leu Pro Thr Leu	312
CAA GCC TCA AGG GAC AGG CCT GCT GGA AAG GAC TTT GTC AGT CCC TCT	1132
Gln Ala Ser Arg Asp Arg Pro Ala Gly Lys Asp Phe Val Ser Pro Ser	328
TCA CCA TCA AGG GGT GTT GGG AAT GTT GGC TGT CCA ATC CAG TTT CCT	1180
Ser Pro Ser Gly Val Gly Asn Val Gly Cys Val Pro Ile Gln Phe Pro	344
ATC ACA GAG GAC CTA GCT GTC ACA TAC CAT CTG ACC TCT GTA TGG TGG	1228
Ile Thr Glu Asp Leu Ala Val Thr Tyr His Leu Thr Ser Val Trp Trp	360
TTT GTG ACT CTG GGG TGATGTGTTG TAAAGCCTCC CTCTCTTTCT CCATACTAAA	1283
Phe Val Thr Leu Gly	365
CAAGTATTAT ATCTCTGTGA ATGAACCAGA CTTTAGTGTT CAGACCAGGC CCTGAACTAT	1343
GTGTGGACTG CTTGTTTTTC TCACACATTT AGAAACTATG GCTTAGAGAG GGAATTCCT	1403
CATATTTTAT CTGATCAATA ACTGACCACC AGATCTCACT AGTTTGACTA AGAATTTCTA	1463
ACCCTCACTA GGTATTTCTA AACTAAACA TGTTTCTAAA CATTTTATC CCTGACTATG	1523

**Fig. 7C**

GCCCAAATAG	TAAATAAAAC	AGCTCAAGCT	TTAGAGGCC	AAGAGACCTA	TGTAAATGTG	1583
TTGGTTAAAA	TAGTTTTTAGA	TAATAAAAGG	GCCCTCAATT	ATTTATGGGC	CTGTCAAGGC	1643
AAAATCTGCA	CAACAGCCAG	TACATCTCAT	TATAAATAAT	TTAGGAGAAG	TGGAATAATC	1703
AGTCAATTAA	GAAAAATGGC	CCTTTATCTA	AAGTTGGCCA	TTTAGATTCA	CGGACTTAT	1763
TCCCTGTTGA	TCTAGGCCAT	GAGAAAACTG	GATAAAAAGT	GGTTTTCAAA	TGTTTTCTTG	1823
GGTATTTGTG	ACTGTTGTCA	TATTTCTTGC	CTTTCCTCTG	TTCTGATATT	CAGGTGCTAT	1883
TGAGAGAGGA	GGAAGGAAGA	AACTAGTCAG	GCAGGCAGTT	AGGTTGGCC	CTCAGTCAAA	1943
TTTCCTTCAA	CAAAAGAAC	GCCTGAAAAA	TCAAACCTGCA	GATAAGGAA	CTTGTACAGG	2003
GGGGCTTGCC	TAAAACATGC	CCACAGCCAC	ATACATTAAA	ACAAGGCTAC	ACAGGAGACT	2063
TGCCCTAGACA	TGCTCACAA	AGAAAATTCC	ATCCCCCTGAC	ACATGCACAG	TAAGGGGAAC	2123
AAAGCCACAT	GGAGTAACTC	AAGCTAAGGG	CTTGCAATGCA	CACATACGAG	ATGGGGTGG	2183
GCTACCAGAA	ATGTGTGCCT	TATGCCCTTTG	TATTCAGCTG	TGAAAATGGCA	ACCCTCTTTT	2243
GGGCCCCCTC	TCTGCAGTGG	AGTGCTTTCT	TCTTTTGTCTT	ATTAAACTTT	CACTTCAACT	2303
TCAAAAAATA	AAAAAATAA	AAAAAATAA				2330

Fig. 7D

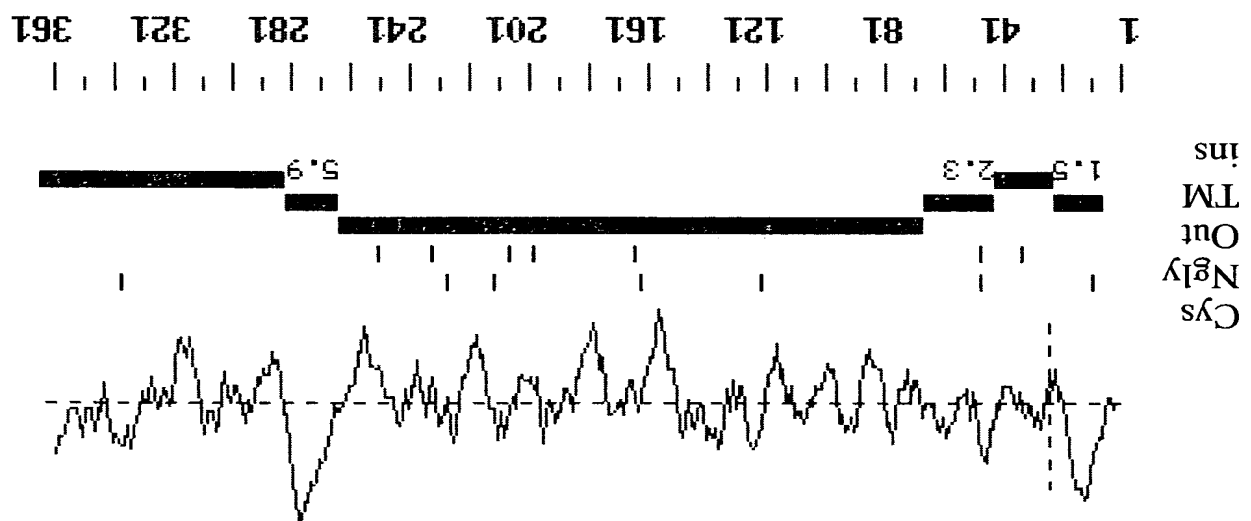


Fig. 8



GAAGTTGAAG	TGAAAGTTTA	ATAAGCAAAA	GAAGAAAGCA	CTCCACTGCA	GAGAGGGGC	2246
GAAGTTGAAG	TGAAAGTTTA	ATAAGCAAAA	GAAGAAAGCA	CTCCACTGCA	GAGAGGGGC	121136
CCAAAGAGG	GTGCCATT	CACAGCTGAA	TACAAAGGCA	TAAGGCACAC	ATTTCTGGTA	2186
CCAAAGAGG	GTGCCATT	CACAGCTGAA	TACAAAGGCA	TAAGGCACAC	ATTTCTGGTA	121196
GCTCCACCC	ATCCTCGTAG	TGTGCATGCA	AGCCCTTAGC	TTGAGTTACT	CCATGTGGCT	2126
GCTCCACCC	ATCCTCGTAG	TGTGCATGCA	AGCCCTTAGC	TTGAGTTACT	CCATGTGGCT	121256
TTGTTCCCT	TACTGTGCAT	GTGTCAGGG	ATGGAATTT	CTATTGTGAG	CATGCTAGG	2066
TTGTTCCCT	TACTGTGCAT	GTGTCAGGG	ATGGAATTT	CTATTGTGAG	CATGCTAGG	121316
CAAGTCTCCT	GTGTAGCCTT	GTTTAAATGT	ATGTGGCTGT	GGCATGTTT	TAGCAAGCC	2006
CAAGTCTCCT	GTGTAGCCTT	GTTTAAATGT	ATGTGGCTGT	GGCATGTTT	TAGCAAGCC	121376
CCCCGTGTACA	AGTTCCCTTA	TCTGCAGTTT	GATTTTTCAG	GCTGTTCTTT	TGTTGAAGG	1946
CCCCGTGTACA	AGTTCCCTTA	TCTGCAGTTT	GATTTTTCAG	GCTGTTCTTT	TGTTGAAGG	121436

**Fig. 9A**

AATTGACTG	AGGGCCACC	CTAACTGCCT	GCCTGACTAG	TTTCTTCCCTT	CCTCCTCTCT	1886
AATTGACTG	AGGGCCACC	CTAACTGCCT	GCCTGACTAG	TTTCTTCCCTT	CCTCCTCTCT	121496
CAATAGCACC	TGAATATCAG	AACCAGAGAA	AGCAAGAAA	TATGACAACA	GTCACAAATA	1826
CAATAGCACC	TGAATATCAG	AACCAGAGAA	AGCAAGAAA	TATGACAACA	GTCACAAATA	121556
CCACAAGAAA	CATTGAAAA	CCACTTTT	TCCAGTTTTC	TCATGGCCTA	GATCCAACAG	1766
CCACAAGAAA	CATTGAAAA	CCACTTTT	TCCAGTTTTC	TCATGGCCTA	GATCCAACAG	121616
GAATAAGTCC	CGTGAATCTA	AATGGCCAAC	TTTAGATAAA	GGGCCATTTT	TCTTAATTGA	1706
GAATAAGTCC	CGTGAATCTA	AATGGCCAAC	TTTAGATAAA	GGGCCATTTT	TCTTAATTGA	121676
CTGATTATTC	CACCTCTCCT	AAATTATT	TAATGAGATG	TACTGGCTGT	TGTGCAGATT	1646
CTGATTATTC	CACCTCTCCT	AAATTATT	TAATGAGATG	TACTGGCTGT	TGTGCAGATT	121736
TTGCCTTGAC	AGGCCATAA	ATAATTGAGG	GCCCTTTTAT	TATCTAAAAC	TATTTTAACC	1586
TTGCCTTGAC	AGGCCATAA	ATAATTGAGG	GCCCTTTTAT	TATCTAAAAC	TATTTTAACC	121796

**Fig. 9B**

AACACATTTA	CATAGGTCTC	TTGGGCCCTCT	AAAGCTTGAG	CTGTTTTTATT	TACTATTGG	1526
AACACATTTA	CATAGGTCTC	TTGGGCCCTCT	AAAGCTTGAG	CTGTTTTTATT	TACTATTGG	121856
GCCATAGTCA	GGGATAAAA	TGTTTAGAAA	CATGTTTTAG	TTTAGAAAATA	CCTAGTGAGG	1466
GCCATAGTCA	GGGATAAAA	TGTTTAGAAA	CATGTTTTAG	TTTAGAAAATA	CCTAGTGAGG	121916
GTTAGAAAATT	CTTAGTCAAA	CTAGTGAGAT	CTGGTGGTCA	GTTATTGATC	AGATAAAAATA	1406
GTTAGAAAATT	CTTAGTCAAA	CTAGTGAGAT	CTGGTGGTCA	GTTATTGATC	AGATAAAAATA	121976
TGAGGAATTC	CCCTCTCTAA	GCCATAGTTT	CTAAATGTGT	GAGAAAAACA	AGCAGTCCAC	1346
TGAGGAATTC	CCCTCTCTAA	GCCATAGTTT	CTAAATGTGT	GAGAAAAACA	AGCAGTCCAC	122036
ACATAGTTCA	GGGCCTGGTC	TGAACACTAA	AGTCTGGTTC	ATTCACAGAG	ATATAATACT	1286
ACATAGTTCA	GGGCCTGGTC	TGAACACTAA	AGTCTGGTTC	ATTCACAGAG	ATATAATACT	122096
TGTTTAGTAT	GGAGAAAGAG	AGGAGGCCTT	TACAACACAT	CACCCACAGAG	TCACAAACCA	1226
TGTTTAGTAT	GGAGAAAGAG	AGGAGGCCTT	TACAACACAT	CACCCACAGAG	TCACAAACCA	122156

**Fig. 9C**

CCATACAGAG	GTCAGATGGT	ATGTGACAGC	TAGGTCCTCT	GTGATAGGAA	ACTGGATTGG	1166
CCATACAGAG	GTCAGATGGT	ATGTGACAGC	TAGGTCCTCT	GTGATAGGAA	ACTGGATTGG	122216
AACACAGCCA	ACATTCCCAA	CACCTGATGG	TGAAGAGGGA	CTGACAAAAGT	CCTTTCAGC	1106
AACACAGCCA	ACATTCCCAA	CACCTGATGG	TGAAGAGGGA	CTGACAAAAGT	CCTTTCAGC	122276
AGGCCTGTCC	CTTGAGGCTT	GTAAGGTTGG	CAGCAGCTGC	TCTAAAAGCT	TTTTACTAGC	1046
AGGCCTGTCC	CTTGAGGCTT	GTAAGGTTGG	CAGCAGCTGC	TCTAAAAGCT	TTTTACTAGC	122336
CCAAGACACA	GGGCTGAACT	TTGCTTTTGA	GCCCCTTACC	TTTTTCCAAG	GAATCAAAAC	986
CCAAGACACA	GGGCTGAACT	TTGCTTTTGA	GCCCCTTACC	TTTTTCCAAG	GAATCAAAAC	122396
AATTAATAAA	ACCAGTCCAA	CACCAATGAA	TGAAATAGGC	CACCAATGAA	TGAAAAAATT	926
AATTAATAAA	ACCAGTCCAA	CACCAATGAA	TGAAATAGGC	CACCAATGAA	TGAAAAAATT	122456
ATCTGTCTTC	TCAGTTTCAG	AA				904
ATCTGTCTTC	TCAGTTTCAG	CA				122478

Fig. 9D

	M	V	2
GGCCCGGCAGCTGCGGCTCGGGATCCGTCGAGGGAGGCCGAGCTTGCCAAAGCTGGCGCCAGCGGGGTC	ATG	GTG	77
P G A R G G G A L A R A A G R G L L A L			22
CCC GGC GCC CGC GGC GGC GCA CTG GCG GCT GCG GGT GGC CTC CTG GCT TTG			137
L L A V S A P L R L Q A E L G D G C G			42
CTG CTC GCG GTC TCC GCC CCG CTC CCG CTG CAG GCG GAG GAG CTG GGT GAT GGC TGT GGA			197
H L V T Y Q D S G T M T S K N Y P G T Y			62
CAC CTA GTG ACT TAT CAG GAT AGT GGC ACA ATG ACA TCT AAG AAT TAT CCC GGG ACC TAC			257
P N H T V C E K T I T V P K G K R L I L			82
CCC AAT CAC ACT GTT TGC GAA AAG ACA ATT ACA GTA CCA AAG GGG AAA AGA CTG ATT CTG			317
R L G D L D I E S Q T C A S D Y L L F T			102
AGG TTG GGA GAT TTG GAT ATC GAA TCC CAG ACC TGT GCT TCT GAC TAT CTT CTC TTC ACC			377
S S S D Q Y G P Y C G S M T V P K E L L			122
AGC TCT TCA GAT CAA TAT GGT CCA TAC TGT GGA AGT ATG ACT GTT CCC AAA GAA CTC TTG			437
L N T S E V T V R F E S G S H I S G R G			142
TTG AAC ACA AGT GAA GTA ACC GTC CGC TTT GAG AGT GGA TCC CAC ATT TCT GGC CGG GGT			497

**Fig. 10A**

F	L	L	L	T	Y	A	S	S	D	H	P	D	L	I	T	C	L	E	R	A	162
TTT	TTG	CTG	ACC	TAT	GCG	AGC	AGC	AGC	GAC	CAT	CCA	GAT	TTA	ATA	ACA	TGT	TTG	GAA	CGA	GCT	557
S	H	Y	L	K	T	E	Y	S	K	F	C	P	A	G	C	C	R	D	V	A	182
AGC	CAT	TAT	TTG	AAG	ACA	GAA	TAC	AGC	AAA	TTC	TGC	CCA	GCT	GGT	GGT	TGT	AGA	GAC	GTA	GCA	617
G	D	I	S	G	N	M	V	D	G	Y	R	D	T	S	L	L	L	C	K	A	202
GGA	GAC	ATT	TCT	GGG	AAT	ATG	GTA	GAT	GGA	TAT	AGA	GAT	ACC	TCT	TTA	TTG	TGC	AAA	GCT	677	
A	I	H	A	G	I	I	A	D	E	L	G	G	Q	I	S	V	L	Q	R	222	
GCC	ATC	CAT	GCA	GGA	ATA	ATT	GCT	GAT	GAA	CTA	GGT	GGC	CAG	ATC	AGT	GTG	CTT	CAG	CGC	737	
K	G	I	S	R	Y	E	G	I	L	A	N	G	V	L	S	R	D	G	S	242	
AAA	GGG	ATC	AGT	CGA	TAT	GAA	GGG	ATT	CTG	GCC	AAT	GGT	GTT	CTT	TCG	AGG	GAT	GGT	TCC	797	
L	S	D	K	R	F	L	F	T	S	N	G	C	S	R	S	L	S	F	E	262	
CTG	TCA	GAC	AAG	CGA	TTT	CTG	TTT	ACC	TCC	AAT	GGT	TGC	AGC	AGA	TCC	TTG	AGT	TTT	GAA	857	
P	D	G	Q	I	R	A	S	S	S	W	Q	S	V	N	E	S	G	D	Q	282	
CCT	GAC	GGG	CAA	ATC	AGA	GCT	TCT	TCC	TCA	TGG	CAG	TCG	GTC	AAT	GAG	AGT	GGA	GAC	CAA	917	
V	H	W	S	P	G	Q	A	R	L	Q	D	Q	G	P	S	W	A	S	G	302	
GTT	CAC	TGG	TCT	CCT	GGC	CAA	GCC	CGA	CTT	CAG	GAC	CAA	GGC	CCA	TCA	TGG	GCT	TCG	GGC	977	

**Fig. 10B**

D	S	S	N	N	H	K	P	R	E	W	L	E	I	D	L	G	E	K	K	322
GAC	AGT	AGC	AAC	AAC	CAC	AAA	CCA	CGA	GAG	TGG	CTG	GAG	ATC	GAT	TTG	GGG	GAG	AAA	AAG	1037
K	I	T	G	I	R	T	T	G	S	T	Q	S	N	F	N	F	Y	V	K	342
AAA	ATA	ACA	GGA	ATT	AGG	ACC	ACA	GGA	TCT	ACA	CAG	TCG	AAC	TTC	AAC	TTT	TAT	GTT	AAG	1097
S	F	V	M	N	F	K	N	N	N	S	K	W	K	T	Y	K	G	I	V	362
AGT	TTT	GTG	ATG	AAC	TTC	AAA	AAC	AAT	AAT	TCT	AAG	TGG	AAG	ACC	TAT	AAA	GGA	ATT	GTG	1157
N	N	E	E	K	V	F	Q	G	N	S	N	F	R	D	P	V	Q	N	N	382
AAT	AAT	GAA	GAA	AAG	GTG	TTT	CAG	GGT	AAC	TCT	AAC	TTT	CGG	GAC	CCA	GTG	CAA	AAC	AAT	1217
F	I	P	P	I	V	A	R	Y	V	R	V	V	P	Q	T	W	H	Q	R	402
TTC	ATC	CCT	CCC	ATC	GTG	GCC	AGA	TAT	GTG	CGG	GTT	GTC	CCC	CAG	ACA	TGG	CAC	CAG	AGG	1277
I	A	L	K	V	E	L	I	G	C	Q	I	T	Q	G	N	D	S	L	V	422
ATA	GCC	TTG	AAG	GTG	GAG	CTC	ATT	GGT	TGC	CAG	ATT	ACA	CAA	GGT	AAT	GAT	TCA	TTG	GTG	1337
W	R	K	T	S	Q	S	T	S	V	S	T	K	K	E	D	E	T	I	T	442
TGG	CGC	AAG	ACA	AGT	CAA	AGC	ACC	AGT	GTT	TCA	ACT	AAG	AAA	GAA	GAT	GAG	ACA	ATC	ACA	1397
R	P	I	P	S	E	E	T	S	T	G	I	N	I	T	T	V	A	I	P	462
AGG	CCC	ATC	CCC	TCG	GAA	GAA	ACA	TCC	ACA	GGA	ATA	AAC	ATT	ACA	ACG	GTG	GCT	ATT	CCA	1457

Fig. 10C

L	V	L	L	V	V	L	V	F	A	G	M	G	I	F	A	A	F	R	K	482
TTG	GTG	CTC	CTT	GTT	GTC	CTG	GTG	TTT	GCT	GGA	ATG	GGG	ATC	TTT	GCA	GCC	TTT	AGA	AAG	1517
K	K	K	K	G	S	P	Y	G	S	A	E	A	Q	K	T	D	C	W	K	502
AAG	AAG	AAG	AAA	GGA	AGT	CCG	TAT	GGA	TCA	GCA	GAG	GCT	CAG	AAA	ACA	GAC	TGT	TGG	AAG	1577
Q	I	K	Y	P	F	A	R	H	Q	S	A	E	F	T	I	S	Y	D	N	522
CAG	ATT	AAA	TAT	CCC	TTT	GCC	AGA	CAT	CAG	TCA	GCT	GAG	TTT	ACC	ATC	AGC	TAT	GAT	AAT	1637
E	K	E	M	T	Q	K	L	D	L	I	T	S	D	M	A	D	Y	Q	Q	542
GAG	AAG	GAG	ATG	ACA	CAA	AAG	TTA	GAT	CTC	ATC	ACA	AGT	GAT	ATG	GCA	GAT	TAC	CAG	CAG	1697
P	L	M	I	G	T	G	T	V	T	R	K	G	S	T	F	R	P	M	D	562
CCC	CTC	ATG	ATT	GGC	ACC	GGG	ACA	GTC	ACG	AGG	AAG	GGC	TCC	ACC	TTC	CGG	CCC	ATG	GAC	1757
T	D	A	E	E	A	G	V	S	T	D	A	G	G	H	Y	D	C	P	Q	582
ACG	GAT	GCC	GAG	GAG	GCA	GGG	GTG	AGC	ACC	GAT	GCC	GGC	GGC	CAC	TAT	GAC	TGC	CCG	CAG	1817
R	A	G	R	H	E	Y	A	L	P	L	A	P	P	E	P	E	Y	A	T	602
CGG	GCC	GGC	CGC	CAC	GAG	TAC	GCG	CTG	CCC	CTG	GCG	CCC	CCG	GAG	CCC	GAG	TAC	GCC	ACG	1877
P	I	V	E	R	H	V	L	R	A	H	T	F	S	A	Q	S	G	Y	R	622
CCC	ATC	GTG	GAG	CGG	CAC	GTG	CTG	CGC	GCC	CAC	ACG	TTC	TCT	GCG	CAG	AGC	GGC	TAC	CGC	1937

**Fig. 10D**

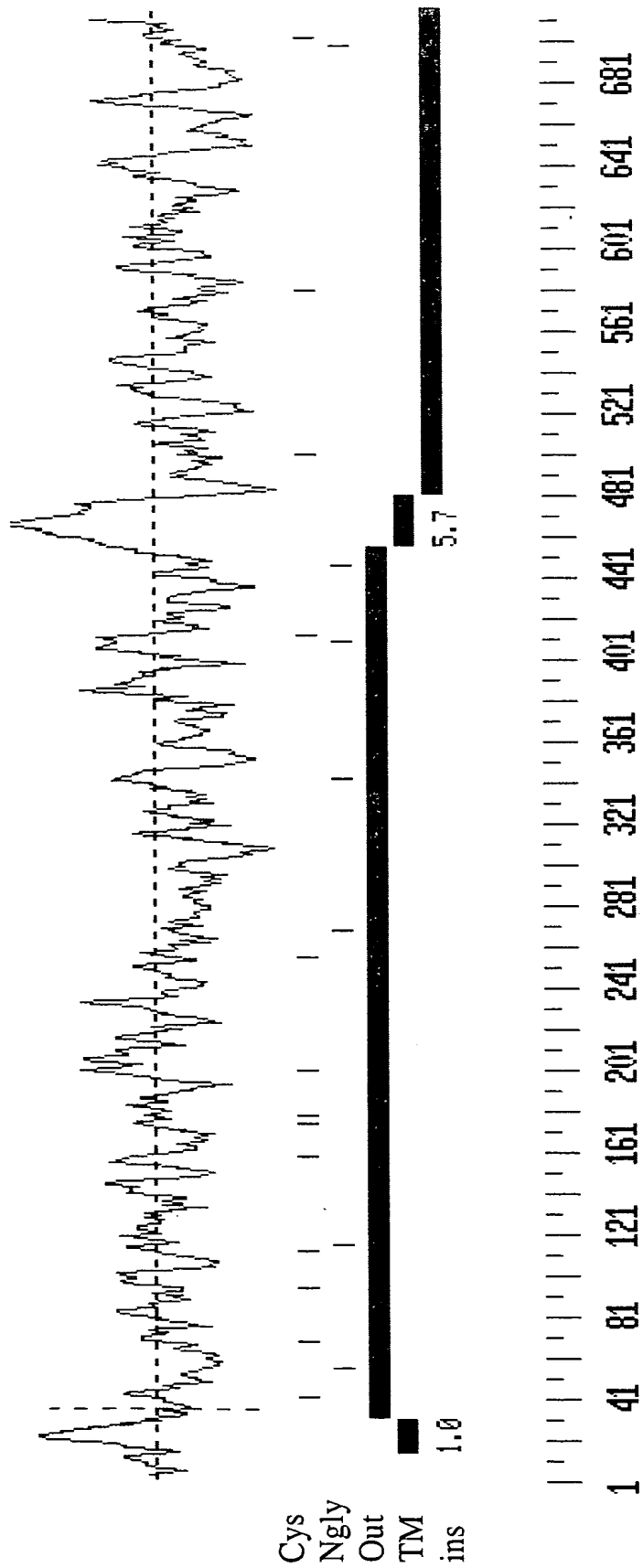


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GCG GGT GTG GGC GCC CAG GAC GGA GAC TAT CAA AGG CCA CAC AGC GCA CAG CCT GCG GAC 2057  
  
R G Y D R P K A V S A L A T E S G H P D 682  
AGG GGC TAC GAC CGG CCC AAA GCT GTC AGC GCC CTC GCC ACC GAA AGC GGA CAC CCT GAC 2117  
  
S Q K P P T H P G T S D S Y S A P R D C 702  
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L T P L N Q T A M T A L L \* 715  
CTC ACA CCC CTC AAC CAG ACG GCC ATG ACT GCC CTT TTG TGA 2219  
  
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CCTGGAAGAAATGAATTACTTGAAGCATGAAAGACACACACAGGTTGTTGTTTATTATTAGCAATTATGACTGTAGATTTA 2851

**Fig. 10E**

AAACAAGCAAAGAAACAACCTCAGCAGCTGCCCGTTTCCTTAGTCTCCACTTCAGAGGGGATGCCAAGAGGTCGG 2930  
 CCCAGCTCCGGTGACCATGAAGGTGGCACAGGAATTACAGTGTGAATGGCTGTGTGCAGATGTTTTCGTACCTCAGATTA 3009  
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 CTGAAAAACAAGTTATTGGAAACATGTTCAATGCAAAAGTGATTCAGACCAAGTCATAAATCGAGCTTTTCTACTGACAT 3167  
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 GACATCAGCTGTACCTCATGCTCAGTAGTTTTTTAATTGAGTTTCTTTTGTGAGTTAACTATGGGAGATTTAAACCTCTTT 3325  
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 AGCTGCTGGTTAGTGTGGAGGGGAAGTGGTTTACTTTGTAGAGTTTACATGGTTTTATGCGGCACACTAATTGTAAATAA 3562  
 CTATGCCAAACCAATAAAAAAATAAAAAA

**Fig. 10F**



**Fig. 10G**



R	E	E	K	R	W	R	W	R	I	N	N	S	V	F	N	G	N	V	T	N	154
CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	ATC	AAC	AAC	TCT	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	640
Q	N	Q	N	F	N	C	A	T	I	G	L	T	K	T	F	D	A	A	S		174
CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA		700
C	D	I	S	Y	R	R	I	C	E	K	N	A	K	*							188
TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	TGT	GAG	AAG	AAT	GCC	AAA	TGA							745
TCACAGTTCCCTGTGACAAAGAACTATACTTGCAACTCTTTTGTGAATCCATACAGGTCGTCTGGCCCAATGATTCTTTTAC																					824
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TGAGCATTTCTGACTGATCAAAAAGGCCCTAGTCTGTTGACAGGGTTTGTATTTTAGCCTCAGAGTATACCATACTA																					1061
CTAGGGAGTAACTGTAGAGTGAGAAATTATAAACATTATTAGGGATTACCATTGGGAAGAGGGATAAACATAGGTCC																					1140
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CCTCAGTCTGAACATAAGGCTTGGCCTTGGGAGGGCTCCTAGTCTGAGCTTGAGCAGCACGGACAGCAGCATTTGTTT																					1298
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CAAAACACACTAGATTTCGTCTTCAGCAAAAGCCCTGAAGAGACACTTAAAGCTAAAATTCCTTGTCTATTTCTGAA																					1456
ACTCCATTATAACATATGTAACTCTTTGTAAACCAAAATTTAGGTAAGCAGGCTTCTTGTCTCTGAAGGTTTGTAGTA																					1535
CCTGGCTGTATTGTGTAGTATTTTAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAAATATATTCATCCCTTC																					1614
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TGGTGCATAAGAAAGAGAAAGAGATGCCTTTTGTGTTTGTAGTAAGAAATAATTAACCATAAAGGAAGACCATGTATAA																					2009
AACTGATGGAAATAATAGTCAACCAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT																					2088

Fig. 11B

ACATGTCAATTGTATATACCAACAAGATTGTTGTAATCATATATTTTATTACAACACATAAGTTCTGCTTCTGCATT 2167  
 CCTAGGTTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTCAGAA 2246  
 CTTGCTTGAAGGAATTACCAGAAGTAATTTGTGTTTGAGATGGGTGGAATTTGGAATTATATAGTAGCCGGTGGAG 2325  
 ATACAAGTTCCTGACTGTGTTGGGAAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA 2404  
 AAATATCAACAGAACTCTAGCCAAAAGGCAAGCCAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTGA 2483  
 GAAGAGAACTGTAGTTGCTTCACTTCCATTTTCATGACAGATAAATCTGCAAACTTTTAAAGATCAGGAAATGTAGACA 2562  
 TCTAGTGATTTCTTAGTAGACAGTTTAATTTCCCCAAGATTAGGAGACACTTCTGTGCAAGTTCTTAAAGTTCCCTGA 2641  
 ATGGCCTGGGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAAGTTTCATCATTTGGGAGAGTTCCCTGGA 2720  
 TCCCTTGCAAGCTTAGATAAATGTGATCTTTATAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTA 2799  
 GCAAGCCACTGAATTTGAGTTTTCACCTTGTTCATATGCTGTGTAATCAGTACAGTTTCTTACCCCTTCTTGGT 2878  
 CTTAAATTTCCCTACTGATAAAATGGGGTAGTAATACCTATCTCAAAAAATATTGCACATATTAAATAACATTCCTCTA 2957  
 TGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTTGAAAGTTGAGATCTTTCATCCAAAGAGTAGCT 3036  
 TTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATA 3115  
 AAAATTTGTGCAAGTCAGAGAAAGGTGCCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGACACACTTTTCATG 3194  
 ACCTCAAAATGTGGCCAGCCTAGGTCAGCCCAACCCCATCCAAACCTTAGACTCACGAACAAATCCACCTGAGATCAG 3273  
 CAGAGCCACCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAACTTATCACTGTAAAAAAAATAAAATAAA 3352  
 GTCTCTCGTATAGCAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTCCCTTTTCGTGTAT 3431  
 TGTTCATCCAGCAACCAGGATGATCTTGTTTAAAAACATTAAACAGATTCTGTCAATCTTTMAAAAAATAAAAGCCATGA 3510  
 AATTNTAGCAAGCCACTGAATTTGAGTTTTCACCTTGGTTTCTAATAATGCTGTGTAATCAGANCAGKTTTCTTACCCT 3589  
 TTCCTTGGTCTTAATTTCTACTGATAAAATGGGTGWTGTAATACCTATCTCAAAAAATTAATGACACATATTARATAACA 3668  
 TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCCAAG 3747  
 AAGTAGCTTTTCAATTTGTSTAGAAGCTTAATGTAGGCAAGCCACTTCAATTTTTCAGAACTTGTTTACTCATTTTATAATA 3826  
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAGGTGCCCTTAAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGACACAC 3905  
 TTTTTCATGACCTCAAAATGTGGGCCAGCCTAGGTCAGCCCAACCCCATCCACCTTAGACTCACGAACAAATCCACCT 3984  
 GAGATCAGCAGAGCCACCTAGATCAGCTGAACCTCTAAGCACAAAAATAAAACTTATCTACTGTAAAAATAAAAAAAA 4063  
 AAAAAAAGAA 4074

Fig. 11C

GTGGTCGGCGGAGGTGAGACTGTGAAGAAGGAACGTTGCTTGGCAAAAGGAGCATATTTCTCAGGAGACGGGC	79
CCCTGCCTGCCACACCAAGCATTAGGCCACCAGGACACCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAG	158
<div style="text-align: center;"> M   N   W   H   M   I   I   S   G   L   I   V   V   V </div>	
GCCCCCTGCAGCTCCTTCATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG	14 220
L   K   V   V   G   M   T   L   F   L   L   Y   F   P   Q   I   F   N   K   S	34
CTT AAA GTT GTT GGA ATG ACC TTA TTT CTA CTT TAT TAT TTC CCA CAG ATT TTT AAC AAA AGT	280
N   D   G   F   T   T   T   R   S   Y   G   T   V   S   Q   I   F   G   S   S	54
AAC GAT GGT TTC ACC ACC ACC AGG AGC TAT GGA ACA GTC TCA CAG ATT TTT GGG AGC AGT	340
S   P   S   P   N   G   F   I   T   T   R   S   Y   G   T   V   C   P   K   D	74
TCC CCA AGT CCC AAC GGC TTC ATT ACC ACA AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC	400
W   E   F   Y   Q   A   R   C   F   F   L   S   T   S   E   S   S   W   N   E	94
TGG GAA TTT TAT CAA GCA AGA TGT TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA	460
S   R   D   F   C   K   G   K   G   S   T   L   A   I   V   N   T   P   E   K	114
AGC AGG GAC TTT TGC AAA GGA AAA GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA	520
L   K   F   L   Q   D   I   T   D   A   E   K   Y   F   I   G   L   I   Y   H	134
CTG AAG TTT CTT CAG GAC ATA ACT GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT	580

**Fig. 11D**

R	E	E	K	R	W	R	W	I	N	N	S	V	F	N	G	K	Y	V	N	154
CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAG	TAC	GTG	AAC	640
M	P	Q	F	P	G	D	L	G	L	L	Q	K	T	K	P	E	I	A	G	174
ATG	CCA	CAG	TTT	CCT	GGG	GAT	CTT	GGT	TTG	CTT	CAA	AAG	ACC	AAA	CCT	GAG	ATT	GCT	GGG	700
F	T	L	E	*																178
TTC	ACC	CTG	GAA	TAG																715
CTCAA	ACGCTGACACTTGACTCTGTTCTGCTCTTCTCCTTCTTCTTCCAA	CCCATCTAT	TCCCTATCTGTCTACCAGTAGC	794																
GGTCC	TGCCCATTTGGGAAACTGAGCTTCTTCTCTGCACTGGGGACTGGATGCTAGCCATCTCCAGGAGACAGGA	873																		
TCAGT	TTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCGGCTTCTGTAGTACTGAGCATTTCTGACTGATCAAAA	952																		
AGGC	TAGTCTGTTGACAGGGTTTGTATTTTAGCCTCAGAGTATACCATACTACTAGGGAGTAAC	TGAGTGAG	1031																	
AAATT	TATAAACATTA	TTTAGGATTACCATG	TGGAAGAGGGATAAACATAGGTCCCTGTGACTTCGTCTCTGTCTCTCAA	1110																
GGGA	ACCCCATTCACATGCCCTCCTAACTCCACAAGCGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACTAAGGCTTGG	1189																		
CCTT	GGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCACGGACAGCATTTGTTTATGGGAATGGAGAGAGTCTGGG	1268																		
CAGGA	TAGGAACCTTCTTGGAGACCCCTTTGAAGAAACAGGCAGCCAAAGGAGCCAAACACACTAGATTTCTGTTCT	1347																		
TCAGC	AAAGCCCTGAAGAGACACTTAAAGCTAA	AAATTCCTTGTCATATTTCTGAAACTCCATTTATAACATATGTAACT	1426																	
CCTT	TGTAACCAAAATTTAGGTAGCAGGCTTCCCTTGTCTCTGAAGGTTTGTAGTACCTGGCTGTATTTGTGAGTATT	1505																		
TTTAA	AAATTTTGATAGTCTCTTAGGCAACAATAATCACAATATATTTCATCCCTTCAGTTC	TGGAGAAAGCCGTGATACC	1584																	
AGGC	CACGCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTTGATCTAGAACTGGTCCAGCCCGCGAAGAG	1663																		
TAGG	AAAAGAGAGAGGGCTGCTCAGGGAAACATTGGCTGGGGCACGGAATAAGCACATAGTAA	AAAGGAAACATCAGGG	1742																	
TCAA	ATGGAAATCACCTGAGACAGGAAACAGGGAGTTCA	TTTGGCCACACTGGAAGAAAGCAAGAAAGAGGAAAGACAA	1821																	
GTC	TTGGAGTACCCCTGGCTGTTCTCCACACTCACAAGACATCAGCTATAC	TCTGCTTGGTGCATAGAAAGAGAAAAAGA	1900																	

**Fig. 11E**



GATGCC	1979
TTTGTG	2058
TTTGTG	2137
TTTGTG	2216
TTTGTG	2295
TTTGTG	2374
TTTGTG	2453
TTTGTG	2532
TTTGTG	2611
TTTGTG	2690
TTTGTG	2769
TTTGTG	2848
TTTGTG	2927
TTTGTG	3006
TTTGTG	3085
TTTGTG	3164
TTTGTG	3243
TTTGTG	3322
TTTGTG	3401
TTTGTG	3480
TTTGTG	3559
TTTGTG	3638
TTTGTG	3717

Fig. 11F

AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTTATAATATGGGAATAAAAAATTTGTGCAAAGT 3796  
CAGAGAAAGGTGCCCTTAAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCAAAATGTGGGC 3875  
CCAGCCTAGGTCAGCCCAACCCCCCATCCAAACCTTAGACTCACGAAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGA 3954  
TCAGCTGAAACTCTAAGCACAAAAATAAAAACTTATCACTGTAAAAAATAAAAAAATAAAAAA 4018

**Fig. 11G**

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCCTGCCACACCA	79
AGCATTAGGCCACCCAGGAAGACCCCCCATCTGTCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTTGCAGCTCCTTC	158
<div> <div>M</div> <div>N</div> <div>W</div> <div>H</div> <div>M</div> <div>I</div> <div>I</div> <div>S</div> <div>G</div> <div>L</div> <div>I</div> <div>V</div> <div>V</div> <div>V</div> <div>L</div> <div>K</div> <div>V</div> <div>V</div> <div>G</div> </div>	19
ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA	218
<div> <div>M</div> <div>T</div> <div>L</div> <div>F</div> <div>L</div> <div>L</div> <div>L</div> <div>Y</div> <div>F</div> <div>P</div> <div>Q</div> <div>I</div> <div>F</div> <div>N</div> <div>K</div> <div>S</div> <div>N</div> <div>D</div> <div>G</div> <div>F</div> <div>T</div> </div>	39
ATG ACC TTA TTT CTA CTT TAT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC ACC	278
<div> <div>T</div> <div>T</div> <div>R</div> <div>S</div> <div>S</div> <div>Y</div> <div>G</div> <div>T</div> <div>V</div> <div>C</div> <div>P</div> <div>K</div> <div>D</div> <div>W</div> <div>E</div> <div>F</div> <div>Y</div> <div>Q</div> <div>A</div> <div>R</div> <div>C</div> </div>	59
ACC ACC AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT	338
<div> <div>F</div> <div>F</div> <div>L</div> <div>S</div> <div>T</div> <div>S</div> <div>E</div> <div>S</div> <div>S</div> <div>W</div> <div>N</div> <div>E</div> <div>S</div> <div>R</div> <div>D</div> <div>F</div> <div>C</div> <div>K</div> <div>G</div> <div>K</div> </div>	79
TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA	398
<div> <div>G</div> <div>S</div> <div>T</div> <div>L</div> <div>A</div> <div>I</div> <div>V</div> <div>N</div> <div>T</div> <div>P</div> <div>E</div> <div>K</div> <div>L</div> <div>L</div> <div>K</div> <div>F</div> <div>L</div> <div>Q</div> <div>D</div> <div>I</div> <div>T</div> </div>	99
GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT	458

**Fig. 11H**

D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W	119
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	518
I	N	N	S	V	F	N	G	N	V	T	N	Q	N	Q	N	F	N	C	A	139
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	578
T	I	G	L	T	K	T	F	D	A	A	S	C	D	I	S	Y	R	R	I	159
ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA	TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	638
C	E	K	N	A	K	*														165
TGT	GAG	AAG	AAT	GCC	AAA	TGA														659
TCACAGT	TCCCCTGTGACAAGAACTATACTTGC	AACTCTTTTGAATCCATACAGGTCG	TCCTGGCCAATGATCTTTTAC	738																
TTACCTAT	CTGTCTACCAAGTAGCGGTCCTTGCCCA	TTTGGAAACTGAGCTTCTTCTCTGCACT	GGGACTGGGATG	817																
CTAGCCAT	CTCCAGGAGACAGGATCAGTTTACGGAA	ACAACACTCAGTTAGTATAGAGATGAGGT	CCGCTTCTGTAGTAC	896																
TGAGCAT	TTCTGACTGATCAAAAAGGCCCTAGTCTG	TTTGACAGGGTTTGTTTATTTAGCCTCAGAG	TATACCATATA	975																
CTAGGGAG	TAACTGTAGAGTGAGAAATTATAAACAT	TATTAGGGATTACCATGGTGAAGAGGATAA	ACATAGGTCC	1054																
TGTGACT	TCGTCCTGTCTCAAGGGAACCCCATTCAC	ATGCCCTCCTAACTCCACAAGCAGGGTAG	CAGAGGCTCT	1133																
CCTCAGT	CTGAACATAAGGCTTGCCCTTGGGGAGG	CTCCTAGTGCTGAGCTTGGAGCAGCACGGAC	CAGCATTGTTT	1212																
ATGGGA	ATGGAGAGGTCCTGGGCAGGATAGGAAC	CTTCTTGAGACCCCTTTGAAGAAACCCAGG	CAGCCAAAGGAGC	1291																
CAACACAC	TAGATTCTGTCTTCAGCAAAAGCCCTGA	AGACACTTAAGCTAAAATTCCTTGTCA	TATTTCTGAA	1370																
ACTCCAT	TATAACATATGTAACTCCTTTGTAA	CCAAAATTTAGGTAAGCAGGCTTCCTTT	GTCTGTAAGGTTTGAGTA	1449																
CCTGGC	TGATTTTGTAGTATTTTAAATTTTGG	ATAGTCTCTTAGGCAACAATAATCACA	TATATTCATCCCTTC	1528																
AGTTCT	GGAGAAAGCCTGATACCAGGCACAGCCT	ACTGTGACCCCAAGGAGCCTGGCACTG	ATTGGCATCACATTGATCTA	1607																

Fig. 11I

GAACTGGTCCAGCCGCGAAGAGTAGGAAAAGAGAAGGGCTGCTCAGGGAAACATTTGGCTGGGGCACGGAAATAAGCAC 1686  
 ATAGTAAAAAGGGAACATCAGGGTCAAAATGGGAAATCACCTGAGACAGGAAACACAGGAGTTTCATTTGGCCACACACTGGAAG 1765  
 AAAGGCAAGAAAGAGGAAGACAAGTCTTGGAGTACCCCTGGCTGTTCTCCACACTCACAAGACATCAGCTATACTCTGCT 1844  
 TGGTGCAATAAGAAAAGAGAAAAGAGATGCCTTTTGTGTTTGTAGTAAGAATAATTAACCCATAAGGAAGACCATGTATAA 1923  
 AACCTGATGGAAATAATAGTCAACCAAAAGTACAGCACATACCATTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT 2002  
 ACATGTCAATTGTAATGTAATACCAAAACAAGATTGTTGTAATCATATTTTATTATTAACAACATAAGTTCCTCTCTGCATT 2081  
 CCTAGGTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAAATTTTAAACATGAGATAACACATCAGGTGTCAGAA 2160  
 CTTGCTTGAAGGGAATTACCAGAAAGTAATTTGTGTTTGAGATGGGTGGAAATTGGAATTATATTAGTAGCCGGTGGAG 2239  
 ATACAAGTTCTCTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAA 2318  
 AAATATCAACAGAACTCTAGCCAAAGGCAAGCCCCAGAACTCAGACAAACAGAAAAGGAAATCCTAATCCTTCTGTTTGA 2397  
 GAAGAGAGAACTGTAGTTGCTTCACCTTCCTATTTCATGACAGAAATAAAGTGCATAACTTTTAAGATCAGGAAAATGTAGACA 2476  
 TCTAGTGATTTCTTTAGTAGACAGATTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAAGGAGCCCA 2555  
 ATGGCCCTGGGGTGGGAGTAGATAGGGAATATGTGGGATTTGGTTTAAAGTTTCATCATTTGGGAGAGTTCCTGGA 2634  
 TCCTTGCAAGCTTAGATAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTTA 2713  
 GCAAGCCACTGAATTTGAGTTTTCACCTTTGTTTCTAATAATGCTGTGTGAAATCAGTACAGTTCCTTACCCCTTCTCTGGT 2792  
 CTTAAATTTCCCTTACTGATAAAAATGGGGTAGTAATACCTATCTCAAAAAATTAATTGCACATATTAAATAACATTCCCTCTA 2871  
 TGTATCTCAATGGCATTAGACATTAGGAGAAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAGAAAGTAGCT 2950  
 TTTCAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTGTTTACTCATTTATATAATATGGGAATA 3029  
 AAAATTTGTGCAAGTCAGAGAAAGGTGCCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGACACACTTTTTCATG 3108  
 ACCTCAAAATGTGGGCCAGCCTAGGTCAAGCCAAACCCCATCCACCTTAGACTCAGCAACAAATCCACCTGAGATCAG 3187  
 CAGAGCCACCCCTAGATCAGCTGAAACTCTAAGCACAAAAATAAAACTTATCAGTAAAAAATAAAAAAATAAAAAA 3266  
 GTCTCTCGTATAGCAAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTTATTGTCCTTTTCGTGTAT 3345  
 TGTTCATCCAGCAACCAGGATGATCTTGTTTAAAAACATTAAACAGATTCTGTCAYKCTTMAAAAAAATAAAAAAGCCATGA 3424  
 AATTNTAGCAAGCCACTGAATTTGAGTTTTCACCTTTGCTTCTAATAATGCTGTGTAATCAGANCAGKTTTCTTACCCCT 3503

**Fig. 11J**

TTCTTGGTC	TTAATT	TCCTT	ACTGATA	AAAA	TGGGT	WGTA	ATA	TACCT	ATCT	CAAAAA	AA	TATT	TGCAC	ATATT	TARATA	AACA	3582									
TTCTCT	TATGT	ATCT	CAAT	GGC	ATT	AGAC	ATT	AGG	ATTT	TGT	GGAG	ATT	TGA	AGTT	GAG	ATCTT	CATCCAAG	3661								
AAGTAG	CTTTT	CAATT	TG	STAG	AA	GC	TTAA	TG	AGG	CAAG	CC	ACTT	CA	TTT	T	CAGAA	CTTGT	TACTCAT	TTATAATA	3740						
TGGGA	ATA	AAAA	ATT	TG	CAAG	TC	AG	AG	GGT	GC	CTT	AAAA	AT	GT	TG	TG	GGC	CAAG	CC	CATGAG	ATCA	AAAG	CACAC	3819		
TTTTC	ATG	ACCT	CA	AA	AT	GT	GGG	CC	CAG	CC	CTA	GGC	CA	AT	CC	CTT	AG	ACT	C	ACG	AA	CA	AAAT	CCACCT	3898	
GAGAT	CAG	CAG	AG	CC	CTA	GAT	CAG	CT	GAA	AA	CTCT	AA	GC	CA	AAAA	ATA	AAAA	CTT	AT	C	ACT	GT	AAAA	AAAA	AAAA	3977
AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	3985

**Fig. 11K**

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCCTGCCACACCA	79
AGCATTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAAGAGGCCCTGCAGCTCCTTC	158
M N W H M I I S G L I V V V L K V V G ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA	19 218
M T L F L L Y F P Q I F N K S N D G F T ATG ACC TTA TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC ACC	39 278
T T R S Y G T V C P K D W E F Y Q A R C ACC ACC AGG AGC TAT GGA ACA GTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT	59 338

**Fig. 11L**

F	F	L	S	T	S	E	S	S	W	N	E	S	R	D	F	C	K	G	K		79
TTT	TTC	TTA	TCC	ACT	TCT	GAA	TCA	TCT	TGG	AAT	GAA	AGC	AGG	GAC	TTT	TGC	AAA	GGA	AAA		398
G	S	T	L	A	I	V	N	T	P	E	K	L	K	F	L	Q	D	I	T		99
GGA	TCC	ACA	TTG	GCA	ATT	GTC	AAC	ACG	CCA	GAG	AAA	CTG	AAG	TTT	CTT	CAG	GAC	ATA	ACT		458
D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W		119
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG		518
I	N	N	S	V	F	N	G	K	Y	V	N	M	P	Q	F	P	G	D	L		139
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAG	TAC	GTG	AAC	ATG	CCA	CAG	TTT	CCT	GGG	GAT	CTT		578
G	L	L	Q	K	T	K	P	E	I	A	G	F	T	L	E	*					155
GGT	TTG	CTT	CAA	AAG	ACC	AAA	CCT	GAG	ATT	GCT	GGG	TTC	ACC	CTG	GAA	TAG					629
CTCAA	ACGCTGACACTTGACTCTGTCTGCTCTTCTCTCTTCTTCTTCCAA	CCCCATCTATTC	CCCTATCTGTCTAC	CAGTAGC																	708
GGTCC	TGCCCCATTTGGGAAACTGAGCTTCTTCTCTGCACTGGGGAC	TGGATGCTAGCCATCTCCAGGACAGGA																			787
TCAGT	TTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTG	TAGTACTGAGCATTTCTGACTGATCAAAA																			866
AGGCCTAGTCTGTTGACAGGGTTTGTGTTTATTTTAGCCCTCAGAGT	ATACCATACTAGGGAGTAACTGTAGAGTGAG																				945
AAATTATAAACATTTATTAGGGATTACCATGGTGAAGAGGGATAAACAT	AGGTCCCTGTGACTTCGTCTCTCTCAA																				1024
GGGAACCCCATTCACATGCCCTCCCTAACTCCACAAGCGAGGTAGCAG	AGGCTCTCCTCAGTCTGAACCTAAGGCTTGG																				1103
CCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCACGGACAGCAT	TGTTATGGGAATGGAGAGAGGTCTGGG																				1182
CAGGATAGGAACCTTCTTGGAGACCCCTTTGAAGAAACCAGGCAGCC	AAAGGAGCCAAACACACTAGATTCTGTCT																				1261
TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAATAATTCCTTGTGCAT	ATTCTGTGAAACTCCATTATAACATATGTA																				1340

**Fig. 11M**



CCTTTGTAACCAAAATTTAGGTAAGCAGGCTTCCTTTGCTCTGAAGGTTTGGAGTACCTGGCTGTATTTGTTGAGTATT 1419  
 TTTAAAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAAATATATTCATCCCTTCAGTTCTGGAGAAAAGCCTGATACC 1498  
 AGGCACAGCCTACTGACCCCAAGAGCCTGGCACTGATTGGCATCACATTTGATCTAGAACTGGTCCAGCCGCCGAAGAG 1577  
 TAGGAAAAGAGAAAGGGCTGCTCAGGGAAACATTTGGCTGGGGCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG 1656  
 TCAAAATGGAAAATCACCTGAGACAGGAAACAGGGAGTTTCATTTGGCCACACTGGAAGAAAGGCAAGAAAGAGGAAGACAA 1735  
 GTCCTGGAGTACCCCTGGCTGTTCTCCACACTCAAGACATCAGCTATACCTCTGCTTGGTGCTATAAGAAAGAGAAAAAGA 1814  
 GATGCCCTTTTGTGTTTGTGAGTAAGAAATAATTAAACCATAAGGAAGACCATGTATAAACTGATGGAATAATAAGTCACC 1893  
 AAAGTACAGCACATACCATTTTGTGCTTAATAACAATGTAGCACAGTAATGACTGTACATGTCTCATTTGTATGTATACCAA 1972  
 ACAAGATTGTTGTAATCATATTTTATTATTAACAACACTAAGTTCTGCTTCTGCATTCCTAGGTTTCATCATTTTGTGGCT 2051  
 CCTTAGCATGGCCACTTACAAATTTTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGA 2130  
 AGTAAATTTGTGTTTGAGATGGGTGGAATTTGGAATTATATTAGTAGCCGGTGGAGATACAAGTTCTCTGACTGTGTTG 2209  
 GGAAGGATAAGTGCTACCGTTGAGAAGGGAAGAAAGGCTGAGTCTAGGTGGAGAAAAAATATCAACAGAACTCTAGCCCA 2288  
 AAGGCAAGCCCCAGAACTCAGACAACTAGCAAAATCCTAATCCTTCTGTTTGTGAGAAAGAGAACTGTAGTTGCTTC 2367  
 ACTTCCCTATTTTCATGACAGAAATACTGCAAACTTTTAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTAGTAGACA 2446  
 GTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAGGAGCCCAATGGCCCTGGGGTGGGAGTGGGGA 2525  
 GTAGATAGGGAATATGTGGGATTTGGTTTAAAGTTTCATCATTTGGGAGAGTTCCCTGGATCCTTGCAAGCTTAGATAAATGT 2604  
 GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAAATTTAGCAAGCCCACTGAATTTGAGTTT 2683  
 CACTTTGTTTCTAATATGCTGTGTAATCAGTACAGTTTCTTACCCCTTCTTGGTCTTAATTTCCCTTACTGATAAAAT 2762  
 GGGGTAGTAATACCTATCTCAAAAATTAATTGCACATATTAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT 2841  
 TAGGAGAAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAGTAGCTTTTCAATTTGCTAGAAGCTTAAT 2920  
 GTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAG 2999  
 GGTGCTTAAAAAATGTTGTGGCCAAGCCACATGAGATCAAGACACACTTTTTCATGACCTCAAAATGTGGGCCCCAGCCTA 3078  
 GGTACGCCAACCCCAACCCCTTAGACTCACGAAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGA 3157  
 AACTCTAAGCACAAAAATAAAACTTATCACTGTAAAAAATAAAAGTCTCTCGTATAGCAAAATCTAA 3236

**Fig. 11N**

CTGATGCAATCTCCATCTGGCC	TCATCCCTTTATTTGTCCTTTCGTGTATTTGTTTCATCCAGCAACCAGGATGA	3315
TCTTGTAAAAACATTAAACAGAT	TCTGTCA YKCTTTMAAAAAAAGCCATGAAATTTNTAGCAAGCCACTGAATTT	3394
GAGTTTTCACCTTTGGTTTCTAA	TATGCTGTGTAATCAGANCAGKTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACT	3473
GATAAAATGGGGTGWGTAA	TACCTATCTCAAAAATATATGCACATATTARATAACATTCCCTCTATGTATCTCAATGGCA	3552
TTAGACATTAGGAGAAAGCA	TTTGTGGAGGATTTTGAAGTTGAGATCTTCATCCCAAGAAGTAGCTTTTCAATTTGSTAGA	3631
AGCTTAATGTAGGCAAGCCAC	TTTCAGAACTTGTTTACTCATTTATAATATGCGAATAAAAAATTTGTGCAAGT	3710
CAGAGAAAGGGTGCCTTAA	AAATGTTGTGGCCCAAGCCACATGAGATCAAGACACACTTTTCATGACCTCAAAATGTGGGC	3789
CCAGCCTAGGTCAGCCAA	CCCCCATCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCTAGA	3868
TCAGCTGAAACTCTAAGCA	CAAAATATAAACTTATCTACTGTAAAAAATAAAAAAAGAACGACCTGCCCCG	3947

**Fig. 110**

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCCTGCCACACCA	79
AGCATTAGGCCACCCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGCCCCCTGCAGCTCCTTC	158
<div> <div>M</div> <div>N</div> <div>W</div> <div>H</div> <div>M</div> <div>I</div> <div>I</div> <div>S</div> <div>G</div> <div>L</div> <div>I</div> <div>V</div> <div>V</div> <div>V</div> <div>L</div> <div>K</div> <div>V</div> <div>V</div> <div>G</div> </div>	19
ATC ATG AAC TGG CAC ATG ATC ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA	218
<div> <div>M</div> <div>T</div> <div>L</div> <div>F</div> <div>L</div> <div>L</div> <div>Y</div> <div>F</div> <div>C</div> <div>P</div> <div>K</div> <div>D</div> <div>W</div> <div>E</div> <div>F</div> <div>Y</div> <div>Q</div> <div>A</div> <div>R</div> <div>C</div> </div>	39
ATG ACC TTA TTT CTA CTT TAT TTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT	278
<div> <div>F</div> <div>F</div> <div>L</div> <div>S</div> <div>T</div> <div>S</div> <div>E</div> <div>S</div> <div>S</div> <div>W</div> <div>N</div> <div>E</div> <div>S</div> <div>R</div> <div>D</div> <div>F</div> <div>C</div> <div>K</div> <div>G</div> <div>K</div> </div>	59
TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA	338

**Fig. 11P**

G	S	T	L	A	I	V	N	T	P	E	K	L	K	F	L	Q	D	I	T	79
GGA	TCC	ACA	TTG	GCA	ATT	GTC	AAC	ACG	CCA	GAG	AAA	CTG	AAG	TTT	CTT	CAG	GAC	ATA	ACT	398
D	A	E	K	Y	F	I	G	L	I	Y	H	R	E	E	K	R	W	R	W	99
GAT	GCT	GAG	AAG	TAT	TTT	ATT	GGC	TTA	ATT	TAC	CAT	CGT	GAA	GAG	AAA	AGG	TGG	CGT	TGG	458
I	N	N	S	V	F	N	G	N	V	T	N	Q	N	Q	N	F	N	C	A	119
ATC	AAC	AAC	TCT	GTG	TTC	AAT	GGC	AAT	GTT	ACC	AAT	CAG	AAT	CAG	AAT	TTC	AAC	TGT	GCG	518
T	I	G	L	T	K	T	F	D	A	A	S	C	D	I	S	Y	R	R	I	139
ACC	ATT	GGC	CTA	ACA	AAG	ACA	TTT	GAT	GCT	GCA	TCA	TGT	GAC	ATC	AGC	TAC	CGC	AGG	ATC	578
C	E	K	N	A	K	*														145
TGT	GAG	AAG	AAT	GCC	AAA	TGA														599
TCACAGT	CCCCTGTGAC	AACTATAC	TTGCA	AACTCT	TTTTTGA	ATCCATAC	AGGTCGTCTGG	CCAAATGAT	TCTTTTAC											678
TTACCTA	TCTGTCTAC	CAGTAG	CGGTCC	TTGCC	CAATTTGGG	AAACTGAG	CTTCTTCT	TCTGCAC	TGGGG	ACTGGG	GACTGG	GATG								757
CTAGCCAT	CTCCAGG	AGACAGG	ATCAG	TTTAC	GGAAAC	AACTCAG	TTAGT	ATAGAG	ATGAG	TCCG	CTTCTGT	AGTAC								836
TGAGCA	TTTCTGACT	GATCA	AAAAGG	CCCTAG	CTGTG	TGACAG	GGTTTGT	TTTATTTAG	CCCTCAG	AGTATAC	CATACTA									915
CTAGGGAG	TAACTGTAG	AGTGAG	AAATT	TATAA	ACATT	ATTAG	GGATT	ACCAT	TGTTG	GAAG	GGATA	AAACAT	AGGTCC							994
TGTGACT	TCGTCTGT	TCTCA	AGGA	ACCC	ATTC	ACATG	CCCCCTC	CTAACT	CCAC	AGCG	AGGTAG	CAGAG	CTCT							1073
CCTCAG	TCTGA	ACTA	AGGCT	TGGC	CTTGGG	AGGCT	CTAG	TGCTG	AGCTT	GGAG	CACG	ACAG	CATG	TTT						1152
ATGGGA	ATGGAG	AGGCT	CTGGC	CAG	GATAG	GAAC	CTTCT	TGGAG	ACCCCTT	TGA	AGAA	AAAC	CAGC	AGC	CAAGG	GAGC				1231

**Fig. 11Q**

CAAACACACTAGATTTCTGTCTTTCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTTCATATTTCTGTAA  
 1310  
 ACTCCATTATAACATATGTAACTCCTTTGTAAACCAAAATTTAGGTAAGCAGGCTTCCTTTTGCTCTGAAGGTTTTTGAGTA  
 1389  
 CCTGGCTGTATTTTGTGAGTATTTTAAAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAATATATTTCATCCCCTTC  
 1468  
 AGTTCTGGAGAAAAGCCCTGATACCAGGCACAGCCCTACTGACCCCAAGAGAGCTGGCACTGATTGGCATCACATTGATCTA  
 1547  
 GAACTGGTCCAGCCCGGAAGAGTAGGAAAAGAGAAGGGCTGCTCAGGGAAACATTTGGCTGGGGCCAGGAATAAGCAC  
 1626  
 ATAGTAAAAAGGGAAACATCAGGGGTCAAATGGAAATCACCTGAGACAGGAAAACAGGGAGTTTCATTTGGCCACACTGGAAG  
 1705  
 AAAGGCAAGAAAGAGGAAGACAAAGTCTTTGGAGTACCCCTGGCTGTTCTCCACACTCACAAGACATCAGCTATACTCTGCT  
 1784  
 TGGTGCATAAGAAAAGAGAAAGAGATGCCCTTTTGTGTTTTTGAGTAAGAAATAATTAAACCATAAGGAAGACCATGTATAA  
 1863  
 AACTGATGGAAATAATAGTCAACCAAGTACAGCACATACCATTTTTGTGTCTAATAACAATGTAGCACAGTAATGACTGT  
 1942  
 ACATGTCATTGTATGTATACCAAAACAAGATTGTTGTAATCATATTTTATTACAACACTAAAGTTCTGCTTCTGCATT  
 2021  
 CCTAGGTTTCATCATTTTGGCTCCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTCAGAA  
 2100  
 CTTGCTTGAAAGGGAATTACCAGAAAGTAAATTGTGTTTTGAGATGGGTGGAAATTGGAAATTATATTAGTAGCCGGTGGAG  
 2179  
 ATACAAAGTTCTGTGACTGTGTTGGGAAAGGATAAGTGCTACCGTTGAGAAAGGGAAGAAAGGCTGAGCTAGGTGGAGAA  
 2258  
 AAATATCAACAGAACTCTAGCCAAAGGCAAGCCCAAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTGA  
 2337  
 GAAGAGAAACTGTAGTTGCTTCACTTCCCTATTTCATGACAGAAATAACTGCAAAACCTTTTAAGATCAGGAAAATGTAGACA  
 2416  
 TCTAGTGATTTCTTTAGTAGACAGTTTAAATTTCCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAAAGGAGCCCA  
 2495  
 ATGGCCCTGGGTGGGAGTGGGAGTAGATAGGGAATATGTGGGATTGTTTAAAGTTTCATCATTTGGGAGAGTTCCCTGGA  
 2574  
 TCCTTGCAAGCTTAGATAAAATGTGATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAAAGGCAATGAAAAATTTA  
 2653  
 GCAAGCCACTGAAATTTGAGTTTTCACCTTTGTTTTCTAAATATGCTGTGTGAATCAGTACAGTTTTTCTTACCCTTTCTTGGT  
 2732  
 CTTAAATTTCCCTTACTGATAAAAATGGGTAGTAATACCTATCTCAAAAAATATTATGCACATATTAAATAACATTCCCTCTA  
 2811  
 TGTATCTCAATGGCATTAGACATTAGGAGAAGCAATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCCAAGAAGTAGCT  
 2890  
 TTTCAAATTTGCTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATAATGGAATA  
 2969  
 AAAATTTGTGCAAGTCAGAGAAGGGTGCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAGACACACTTTTCATG  
 3048  
 ACCTCAAATGTGGGCCAGCCTAGGTCAGCCCAACCCCCATCCCTTAGACTCACGAAACAAATCCACCTGAGATCAG  
 3127

**Fig. 11R**

CAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAA  
 3206  
 GTCTCTCGTATAGCAAAAATCTAACTGATGCAATCTCCATCTGGCCTTCATCCTTCTCCCTTTATTGTCCTTTCGTGTAT  
 3285  
 TGTTCATCCAGCAACCAGGATGATCTTGTTTAAAACATTAAACAGATTCTGTCAYKCTTTMAAAAAAAGCCATGA  
 3364  
 AATTNTAGCAAGCCACTGAATTGAGTTTTCACCTTTGGTTTCTAATAATGCTGTGAATCAGANCAGKTTTCTTACCCCT  
 3443  
 TTCTTGGTCTTAAATTTCCCTTACTGATAAAAATGGGGTWTAAATACCTATCTCAAAAAATTATTGCACATATTARATAACA  
 3522  
 TTCCTCTATGTATCTCAATGGCATTAGACATTAGGAGAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAG  
 3601  
 AAGTAGCTTTTCAATTTGSTAGAAGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTTATAATA  
 3680  
 TGGGAATAAAAAATTTGTGCAAGTCAGAGAAAGGTGCCCTTAAAAATGTTGTGGCCCAAGCCACATGAGATCAAAGACACAC  
 3759  
 TTTTTCATGACCTCAAATGTGGGCCCCAGCCTAGGTCAGCCAAACCCCCATCCAAACCTTAGACTCACGAACAAATCCACCT  
 3838  
 GAGATCAGCAGAGCCACCCTAGATCAGCTGAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAA  
 3917  
 AAAAAAA  
 3925

**Fig. 11S**

GAGACTGTGAAGAAGAAACGTTGCTTGGGCAAAAGGAGCATATTTCTCAGGAGACGGGGCCCTGCCTGCCACACCA	79
AGCATTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCTTCCAGGGAGAAAGAGGCCCTGCAGCTCCTTC	158
<div>M N W H M I I S G L I V V L K V V G</div> <div>ATC ATG AAC TGG CAC ATG ATC ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA</div>	<div>19</div> <div>218</div>
<div>M T L F L L Y F C P K D W E F Y Q A R C</div> <div>ATG ACC TTA TTT CTA CTT TAT TTC TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT</div>	<div>39</div> <div>278</div>
<div>F F L S T S E S S W N E S R D F C K G K</div> <div>TTT TTC TTA TCC ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA</div>	<div>59</div> <div>338</div>
<div>G S T L A I V N T P E K L K F L Q D I T</div> <div>GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG AAG TTT CTT CAG GAC ATA ACT</div>	<div>79</div> <div>398</div>
<div>D A E K Y F I G L I Y H R E E K R W R W</div> <div>GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT CGT GAA GAG AAA AGG TGG CGT TGG</div>	<div>99</div> <div>458</div>
<div>I N N S V F N G K Y V N M P Q F P G D L</div> <div>ATC AAC AAC TCT GTG TTC AAT GGC AAG TAC GTG AAC ATG CCA CAG TTT CCT GGG GAT CTT</div>	<div>119</div> <div>518</div>
<div>G L L Q K T K P E I A G F T L E *</div> <div>GGT TTG CTT CAA AAG ACC AAA CCT GAG ATT GCT GGG TTC ACC CTG GAA TAG</div>	<div>135</div> <div>569</div>

**Fig. 11T**

CTCAAACGCTGACACTTGACTCTGTGTTCTGCTCTTCTCTCCCTTTCTTCCAACCCATCTATTCCCTATCTGTCTACCAGTAGC 648  
 GGTCCCTTGCCCATTTGGGAAACTGAGCTTCTTTCTTGCACTGGGGACTGGATGCTAGCCATCTCCAGGAGACAGGA 727  
 TCAGTTTTACGGAAACAACCTCAGTTAGTATAGAGATGAGGTCCGCTTCTGTAGTACTGAGCAATTTCTGACTGATCAAAA 806  
 AGCCCTAGTCTGTGACAGGGTTTGTATTTTATTTTAGCCCTCAGAGTATACCATACTACTAGGGAGTAACTGTAGAGTGAG 885  
 AAATTATAAAACATTTATTAGGGATTACCATGGTGGAAAGAGGGATAAACATAGGTCCTGTGACTTCGTCTCTGTTCTCAA 964  
 GGGAAACCCCATTCACATGCCCCCTCCTAACCTCCAAGCGAGGGTAGCAGAGGCTCTCCTCAGTCTGAACATAAGGCTTGG 1043  
 CCTTGGGAGGGCTCCTAGTGTGAGCTTGGAGCAGCACGGACAGCAATGTTTATGGGAATGGAGAGAGGTCCTGGG 1122  
 CAGGATAGGAAACCTTCTTGGAGACCCCTTTGAAGAAAACCCAGGCAGCCAAAGGAGCCAAACACACTAGATTTCGTGTTCT 1201  
 TCAGCAAAGCCCTGAAGAGACACTTAAGCTAAAAATTCCTTGTCTATATTTCTGAAACTCCCATTTATAACATATGTAACCT 1280  
 CCTTTGTAAACCAAATTTAGGTAAGCAGGCTTCCCTTGTCTGTGAAGGTTTGTAGTACCTGGCTGTATTTTGTGTGAGTATT 1359  
 TTTAAATTTTGGATAGTCTCTTAGGCAACAATAATCACAAATATATTTCATCCCTTCAGTTCTGGAGAAAAGCCTGATACC 1438  
 AGGCACAGCCTACTGACCCCAAGGAGCCTGGCACTGATTGGCATCACATTTGATCTAGAACTGGTCCAGCCGCCGAAGAG 1517  
 TAGGAAAAGAGAAAGGCTGCTCAGGGAAAACATTTGGCTGGGGCACGGAATAAGCACATAGTAAAAAGGGAACATCAGGG 1596  
 TCAAAATGGAAATCACCTGAGACAGGAAACAGGGAGTTTCATTTGGCCACACTGGAGAAAGCAAGGAAAGAGGAAGACAA 1675  
 GTCTTGGAGTACCCCTGGCTGTTCTCCACACTCAACAAGACATCAGCTATATACTCTGCTTGGTGCATAAGAAAAGAGAAAAGA 1754  
 GATGCCCTTTTGTGTTTGTAGTAAGAAATAATTAACCATTAAGGAAGACCATGTATAAAACTGATGGAATAATAGTCACC 1833  
 AAAGTACAGCACATACCATTTTGTGTCATAATAACAATGTAGCACAGTAATGACTGTACATGTTCATTTGTATGTATACCAA 1912  
 ACAAGATTGTTGTAAATCATATTTTATTTTATTAACAACATAAGTTCTGTCTTCTGCAATTCCTAGGTTTCATCATTTTGGCT 1991  
 CCTTAGCATGGCCACTTACAATTTTAAACATGAGATAACACATCAGGTGTCAGAACTTGCTTGAAGGGAATTACCAGA 2070  
 AGTAAATTTGTGTTTGAGATGGGTGGAATTTGGAATTTATATTAGTAGCCGGTGGAGATACAAAGTTCTCTGACTGTGTTG 2149  
 GGAAAGGATAAGTGCTACCGTTGAGAAAGGAAGAGCTGAGTCTAGGTGGAGAAAAATATCAACAGAACTCTAGCCA 2228  
 AAGGCAAGCCCCAGAACTCAGACAAACAGAAAGGAAATCCTAATCCTTCTGTTTGTAGAGAGAGAACTGTAGTTGCTTC 2307  
 ACTTCCCTATTTCATGACAGAATAACTGCAAACTTTTAAAGATCAGGAAATGTAGACATCTAGTGATTTCTTTTAGTAGACA 2386

**Fig. 11U**



GTTTAATTTCCCCAAGATTAGGAGACACTTCTGTGCAGGTTCTAAAGGAGCCCCAATGGCCTGGGGTGGAGTGGGGA 2465  
 GTAGATAGGGAATATGTGGGATTTGGTTTAAGTTCATCATTTGGGAGAGTTCTCTGGATCCTTGCAAGCTTAGATATAAATGT 2544  
 GATCTTTATTAGATAGCAGTGGCATGCTTTTAAAAAAGGCAATGAAAATTTAGCAAGCCACTGAATTTGAGTTTT 2623  
 CACTTTGTTTCTAATATGCTGTGTGAATCAGTACAGTTTCTTACCCTTTCTTGGTCTTAATTTCCCTTACTGATAAAAT 2702  
 GGGGTAGTAATACCTATCTCAAAAAATTATTGCACATATTAAATAACATTCCTCTATGTATCTCAATGGCATTAGACAT 2781  
 TAGGAGAAGCATTTTGTGGAGGATTTTGAAGTTGAGATCTTTCATCCAAAGAGTAGCTTTTCAATTTGCTAGAAGCTTAAT 2860  
 GTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGTCAGAGAAG 2939  
 GGTGCCCTTAAAAATGTTGTGGCCAAGCCCATGAGATCAAGACACACACTTTTCATGACCTCAAATGTGGGCCCAGCCTA 3018  
 GGTGAGCCAAACCCCATCCAAACCTTAGACTCACGAAACAAATCCACCTGAGATCAGCAGAGCCACCCTAGATCAGCTGA 3097  
 AACTCTAAGCACAAAAATAAAAACTTATCCTGTATAAAAAAAGTCTCTCGTATAGCAAAATCTAA 3176  
 CTGATGCAATCTCCATCTGGCCCTTCATCCCTTATTTGTCCCTTTCGTGTATTGTTTCATCCAGCAACCAGGATGA 3255  
 TCTTGTAAAAACATTAACAGATTCTGTCA YKCTTTTMAAAAAAAGCCCATGAAAATTNTAGCAAGCCACTGAAATTT 3334  
 GAGTTTTCACCTTTGTTTCTAATATGCTGTGTGAATCAGANCAGKTTTCTTACCCCTTTCTTGGTCTTAATTTCCCTTACT 3413  
 GATAAAATGGGGTGTAAATACCTATCTCAAAAAATTATTGCACATATTARATAACATTCCTCTATGTATCTCAATGGCA 3492  
 TTAGACATTAGGAGAAGCATTTTGTGGAGGATTTGAAGTTGAGATCTTCATCCAAAGAGTAGCTTTTCAATTTGSTAGA 3571  
 AGCTTAATGTAGGCAAGCCACTTCATTTTTCAGAACTTGTTTTACTCATTTATAATATGGGAATAAAAAATTTGTGCAAGT 3650  
 CAGAGAAGGGTGCCCTTAAAAATGTTGTGGCCAAGCCCATGAGATCAAGACACACACTTTTCATGACCTCAAATGTGGGC 3729  
 CCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCACGAAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGA 3808  
 TCAGCTGAAAACCTTAAGCACAAAAATAAAAACTTATCACTGTAAAAAAGTAAAAAAGAAAGCACCTGCCCCG 3887  
 GCGGGCCGCC 3898

**Fig. 11V**

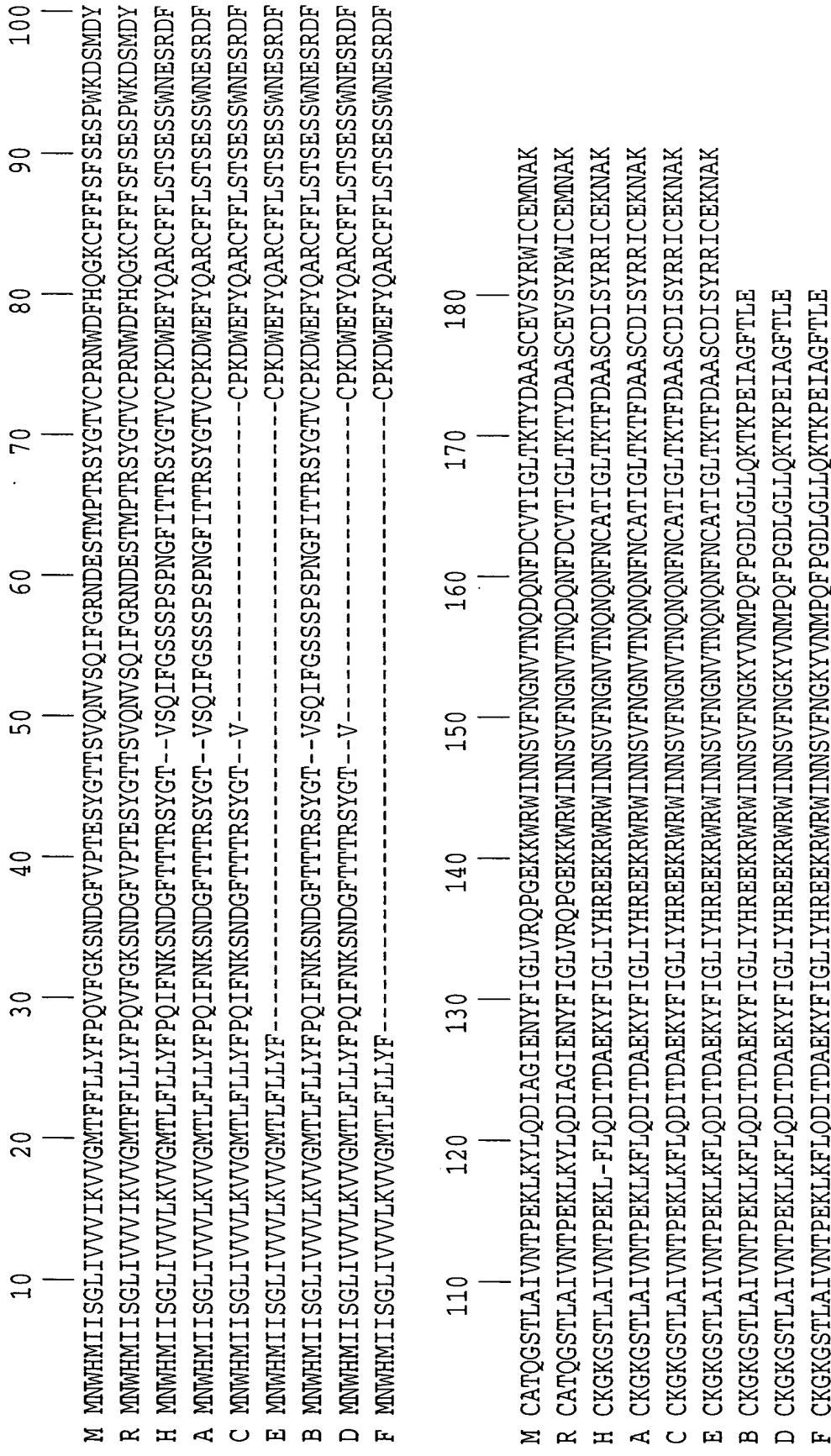


Fig. 11W

	10	20	30	40	50	60	70	80	90	100
A	GTGGTCGGCCGAGGTGAGACTGTGAAGAAGGAAGAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
B	GTGGTCGGCCGAGGTGAGACTGTGAAGAAGGAAGAACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
C	GAGACTGTGAAGAAGGAAG-----AACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
D	GAGACTGTGAAGAAGGAAG-----AACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
E	GAGACTGTGAAGAAGGAAG-----AACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									
F	GAGACTGTGAAGAAGGAAG-----AACGTTGCTTGGGCAAAAGGAGCATATTCTCAGGAGACGGGGCCCCCTGCCTGCCACACCAAGCA									

	110	120	130	140	150	160	170	180	190	200
A	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCCTCCAGGGAGAAAAGAGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
B	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCCTCCAGGGAGAAAAGAGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
C	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCCTCCAGGGAGAAAAGAGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
D	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCCTCCAGGGAGAAAAGAGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
E	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCCTCCAGGGAGAAAAGAGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									
F	TTAGGCCACCAGGAAGACCCCCCATCTGCAAGCAAGCCTAGCCCTCCAGGGAGAAAAGAGCCCCCTGCAGCTCCTTCATCATGAACCTGGCACATGATCATCT									

	210	220	230	240	250	260	270	280	290	300
A	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAAATGACCTTATTCTACTTTTATTTCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACCAC									
B	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAAATGACCTTATTCTACTTTTATTTCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACCAC									
C	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAAATGACCTTATTCTACTTTTATTTCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACCAC									
D	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAAATGACCTTATTCTACTTTTATTTCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACCAC									
E	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAAATGACCTTATTCTACTTTTATTTCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACCAC									
F	CTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAAATGACCTTATTCTACTTTTATTTCCACAGATTTTAAACAAAAGTAACGATGGTTTCACCCACCAC									

**Fig. 11X-1**

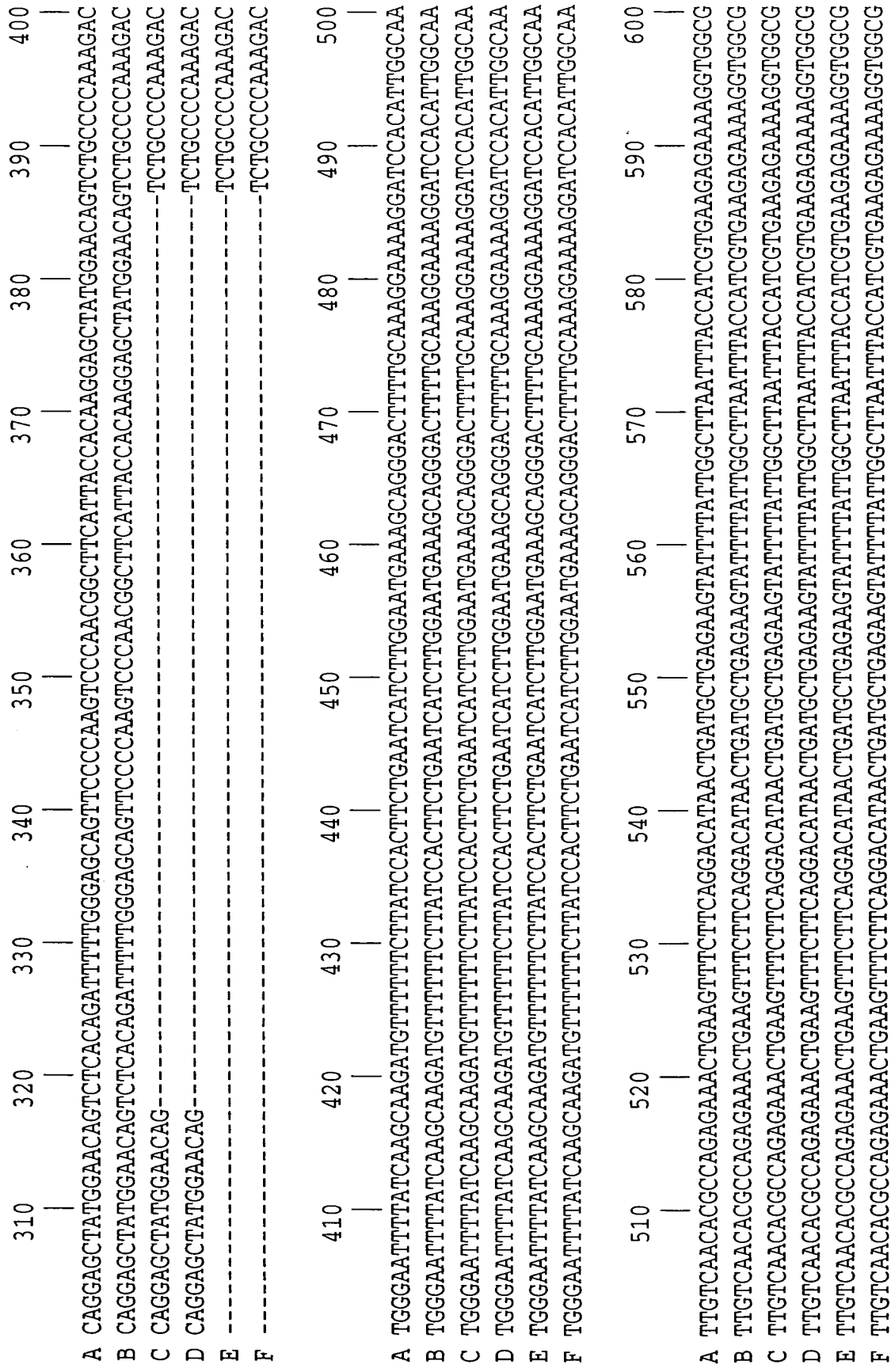


Fig. 11X-2

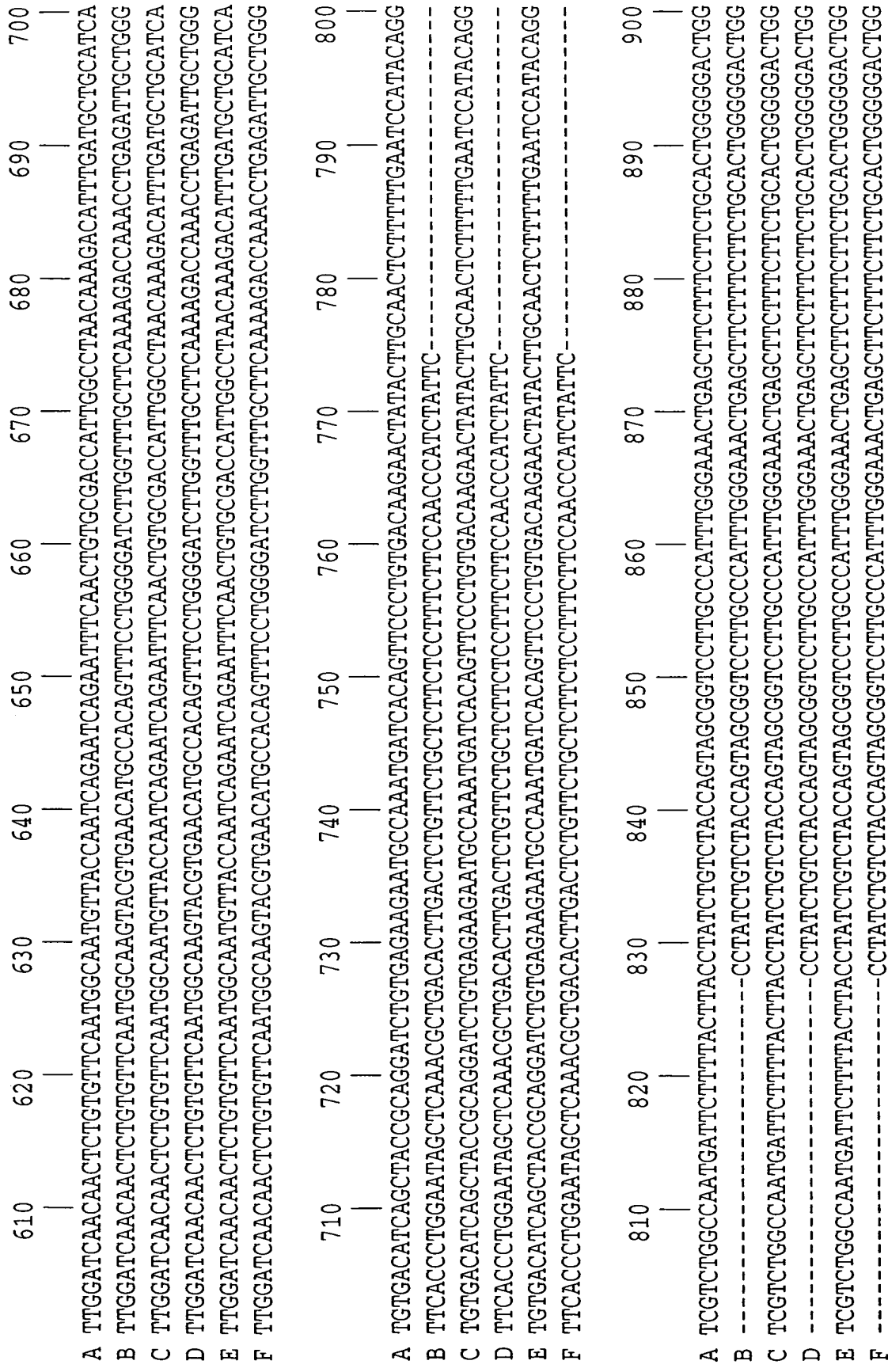
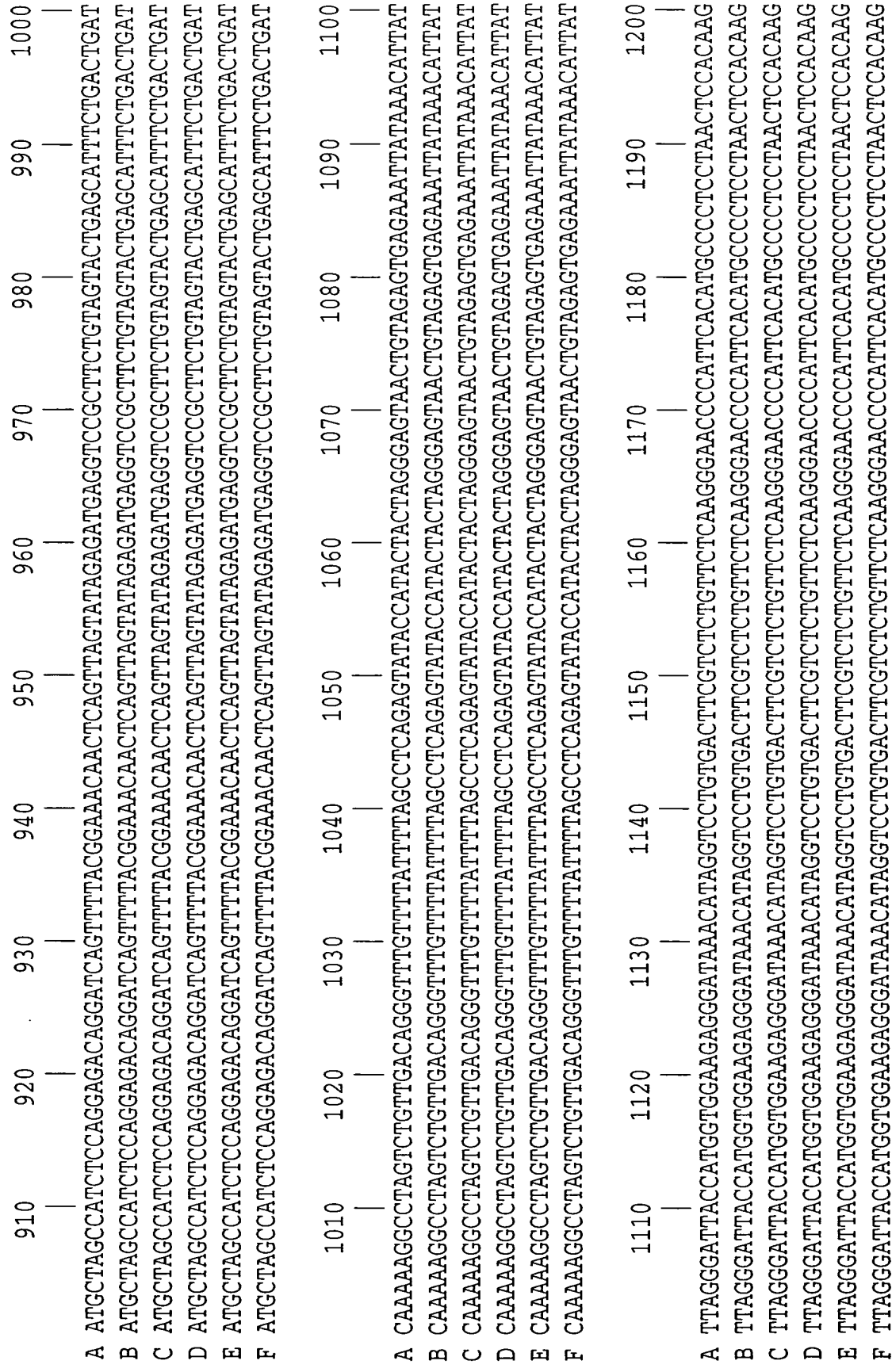
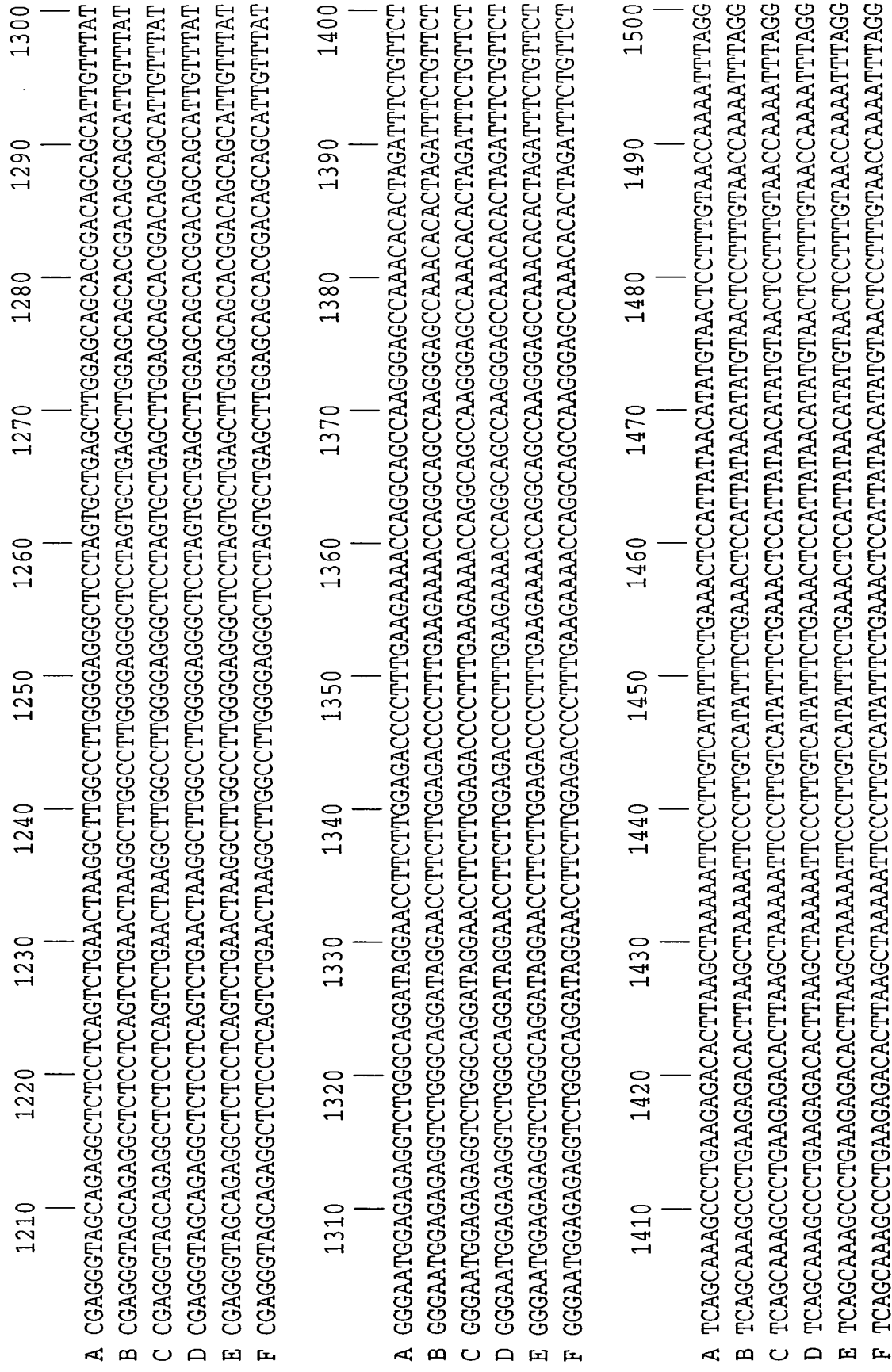
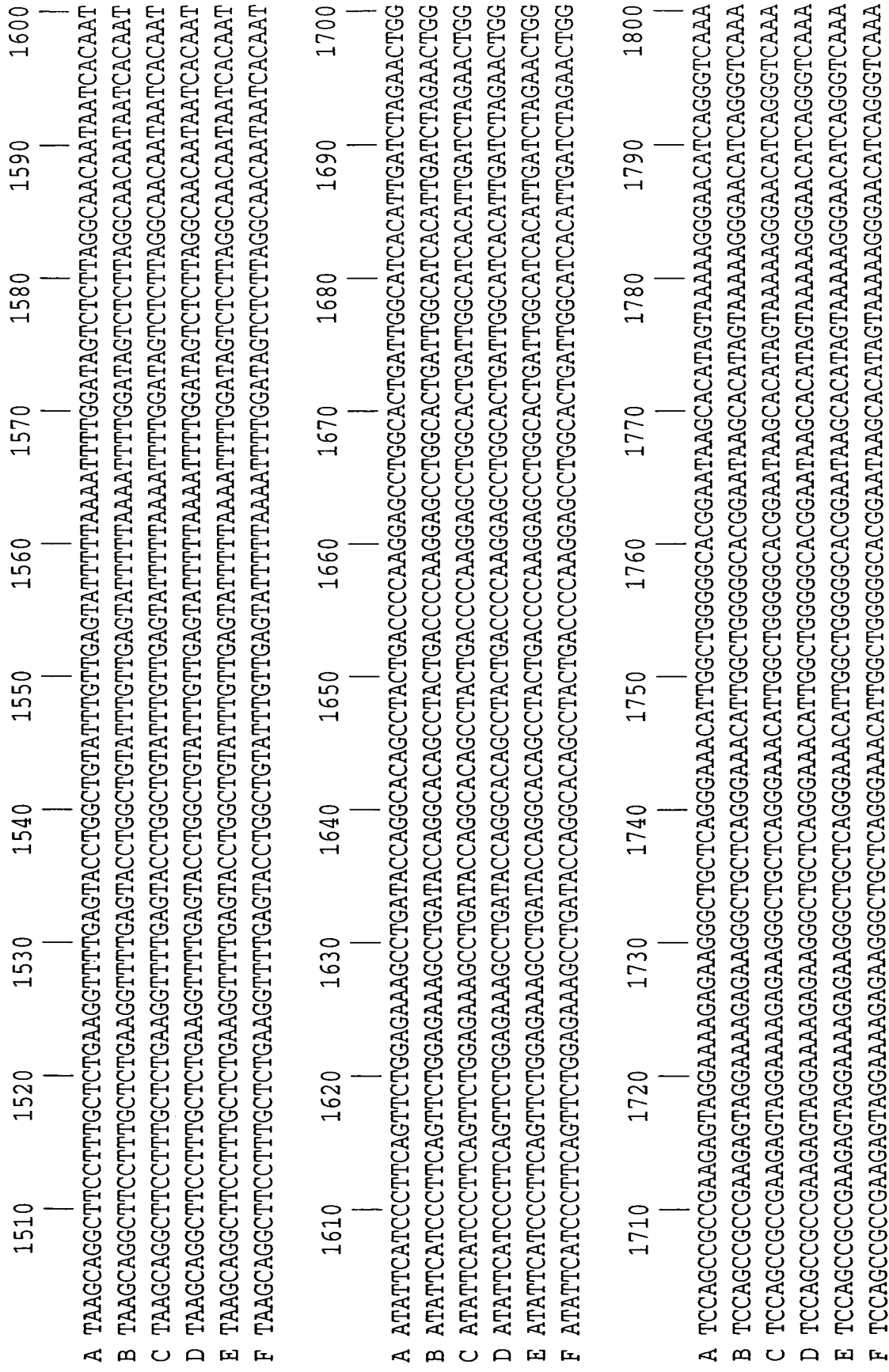


Fig. 11X-3



**Fig. 11X-4**





**Fig. 11X-6**



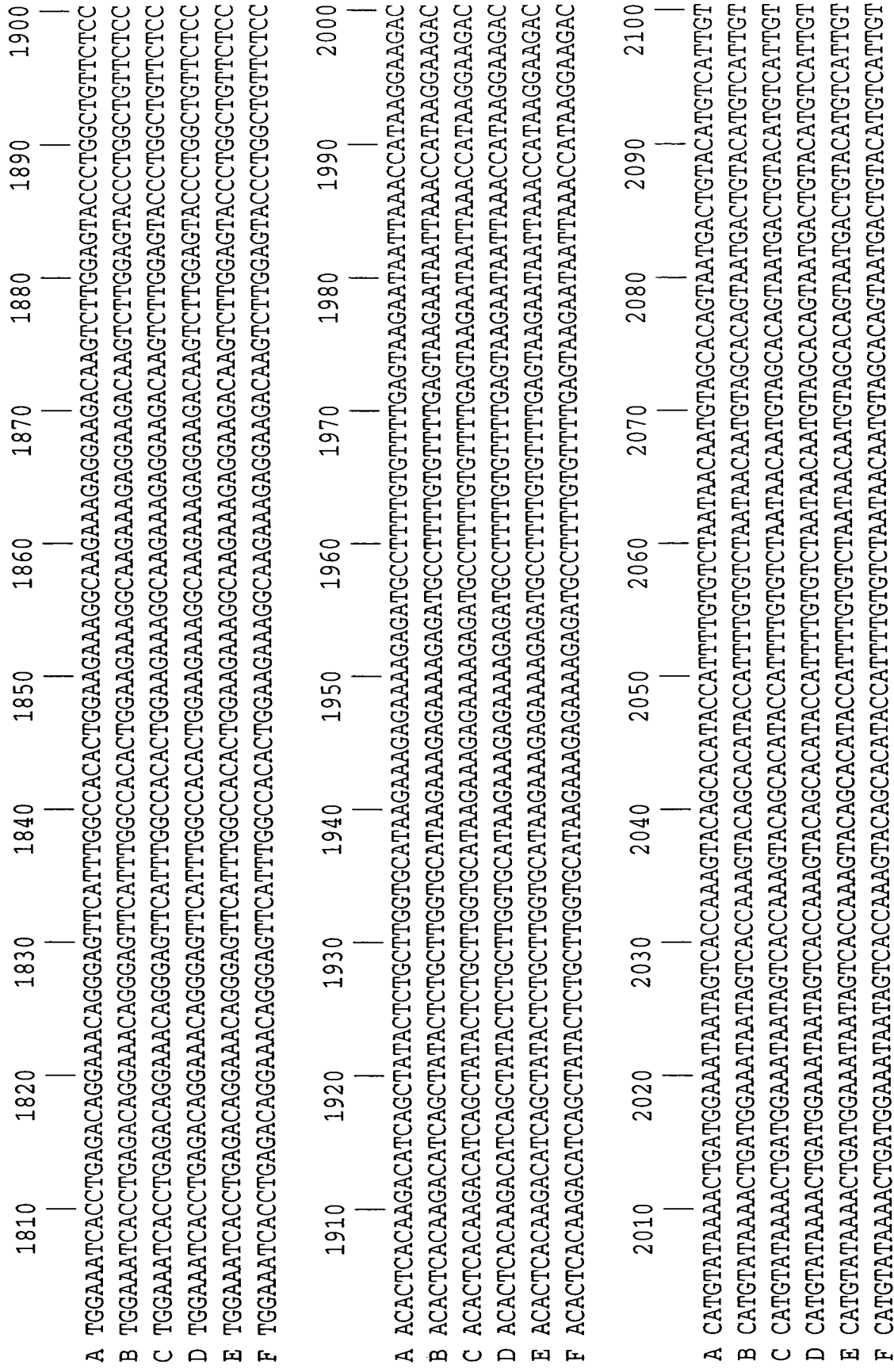
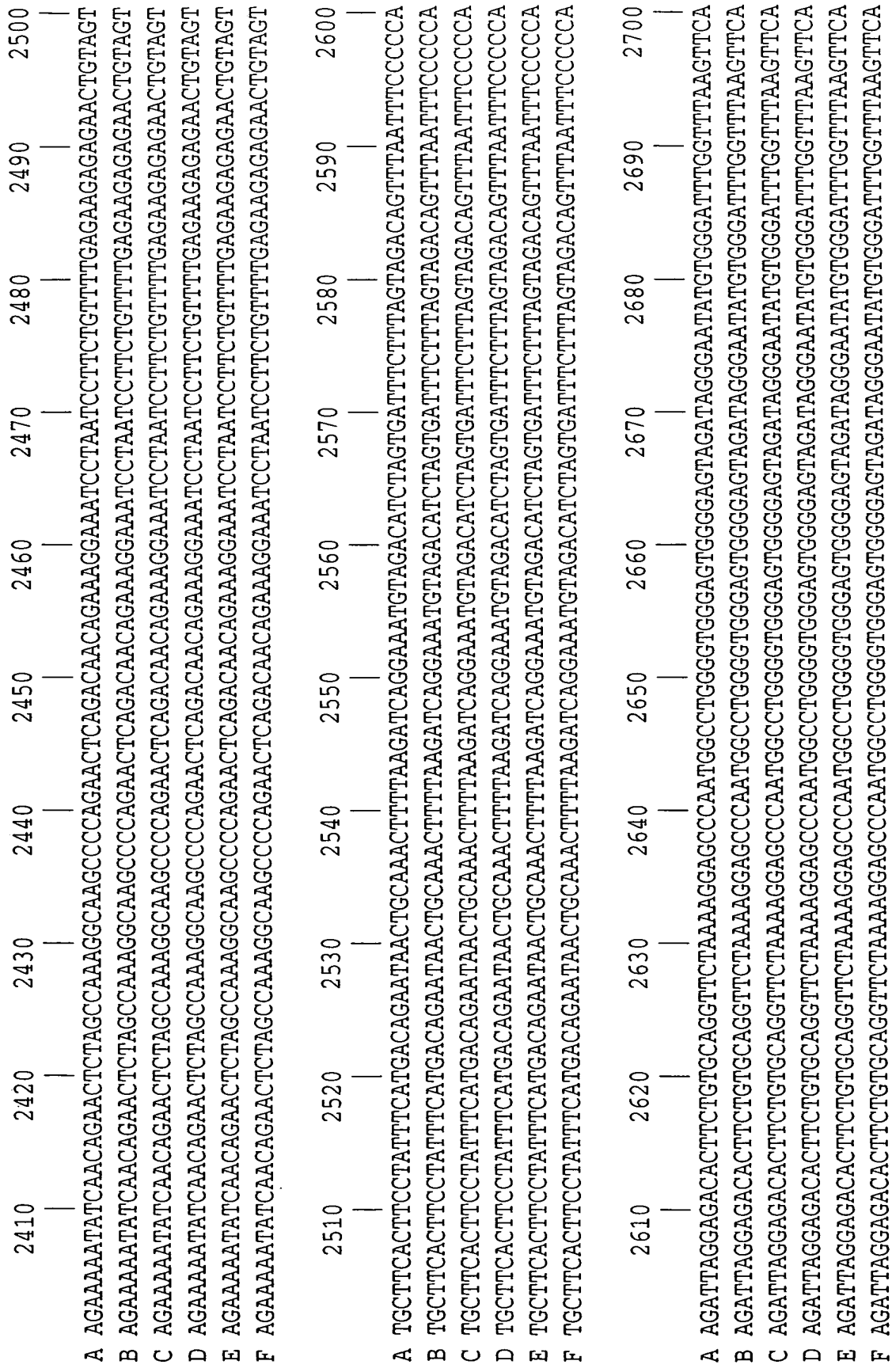


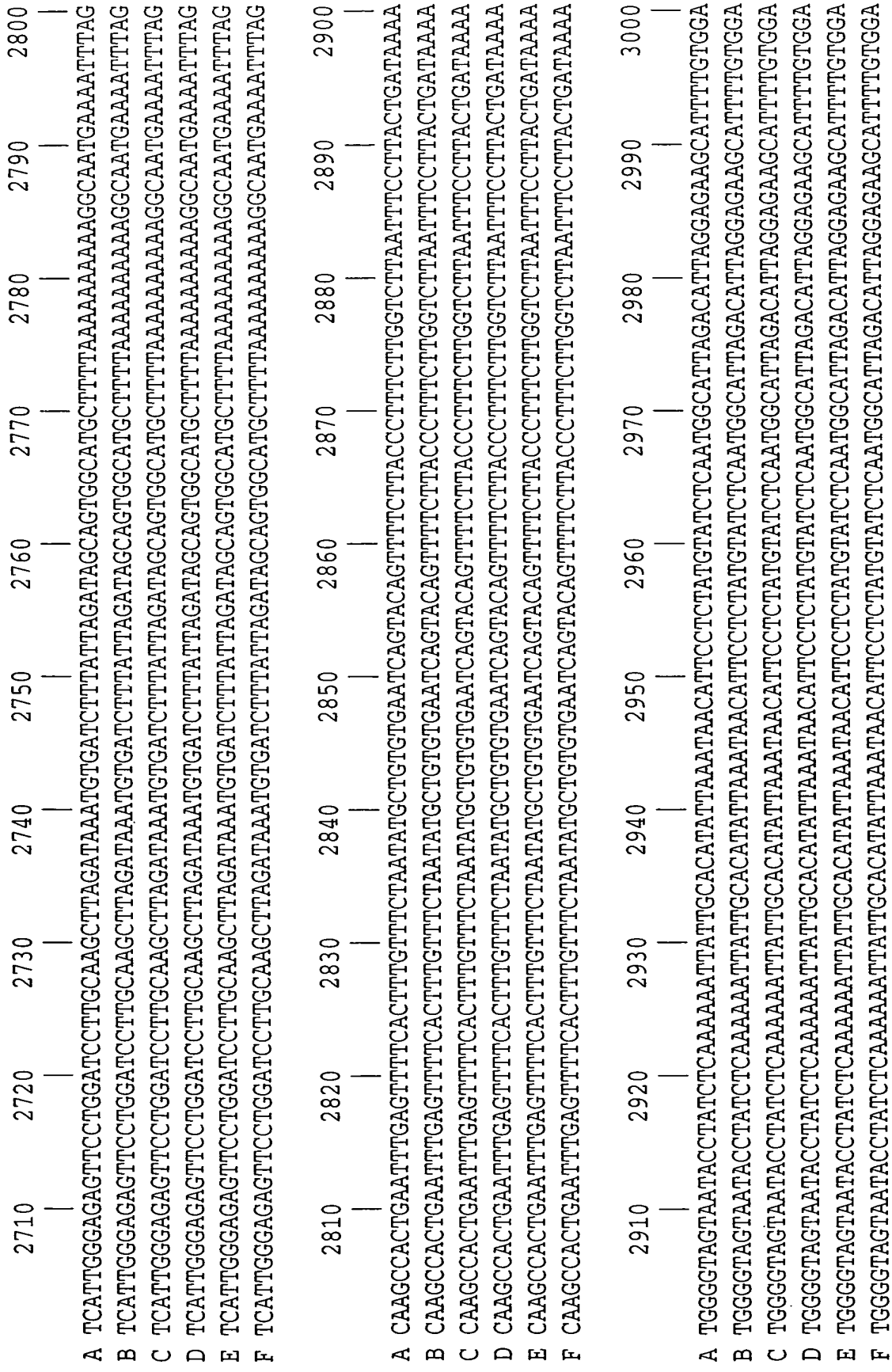
Fig. 11X-7

	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200
A	ATGTATACCAACAAGATTGTTGTA	ATATATTTTATTAACA	CACTAAGTTCTGCTTCTGC	ATTCCCTAGGTTTCATCATTTT	TGGCTCCCTTAGCATG					
B	ATGTATACCAACAAGATTGTTGTA	ATATATTTTATTAACA	CACTAAGTTCTGCTTCTGC	ATTCCCTAGGTTTCATCATTTT	TGGCTCCCTTAGCATG					
C	ATGTATACCAACAAGATTGTTGTA	ATATATTTTATTAACA	CACTAAGTTCTGCTTCTGC	ATTCCCTAGGTTTCATCATTTT	TGGCTCCCTTAGCATG					
D	ATGTATACCAACAAGATTGTTGTA	ATATATTTTATTAACA	CACTAAGTTCTGCTTCTGC	ATTCCCTAGGTTTCATCATTTT	TGGCTCCCTTAGCATG					
E	ATGTATACCAACAAGATTGTTGTA	ATATATTTTATTAACA	CACTAAGTTCTGCTTCTGC	ATTCCCTAGGTTTCATCATTTT	TGGCTCCCTTAGCATG					
F	ATGTATACCAACAAGATTGTTGTA	ATATATTTTATTAACA	CACTAAGTTCTGCTTCTGC	ATTCCCTAGGTTTCATCATTTT	TGGCTCCCTTAGCATG					
	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300
A	GCCACTTACAATTTTAA	CATGAGATAACACAT	CAGGTGTCAGAACTT	GCCTTGAAGGGAATT	TACCAGAA	GTAAATTTGTGTTT	TGAGATGGGGTGGAAATT			
B	GCCACTTACAATTTTAA	CATGAGATAACACAT	CAGGTGTCAGAACTT	GCCTTGAAGGGAATT	TACCAGAA	GTAAATTTGTGTTT	TGAGATGGGGTGGAAATT			
C	GCCACTTACAATTTTAA	CATGAGATAACACAT	CAGGTGTCAGAACTT	GCCTTGAAGGGAATT	TACCAGAA	GTAAATTTGTGTTT	TGAGATGGGGTGGAAATT			
D	GCCACTTACAATTTTAA	CATGAGATAACACAT	CAGGTGTCAGAACTT	GCCTTGAAGGGAATT	TACCAGAA	GTAAATTTGTGTTT	TGAGATGGGGTGGAAATT			
E	GCCACTTACAATTTTAA	CATGAGATAACACAT	CAGGTGTCAGAACTT	GCCTTGAAGGGAATT	TACCAGAA	GTAAATTTGTGTTT	TGAGATGGGGTGGAAATT			
F	GCCACTTACAATTTTAA	CATGAGATAACACAT	CAGGTGTCAGAACTT	GCCTTGAAGGGAATT	TACCAGAA	GTAAATTTGTGTTT	TGAGATGGGGTGGAAATT			
	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
A	GGAATTATATTAGT	AGCCGGTGGAGATACA	AGTTCTCTGACTGT	GTGGGAAAGGATAAGT	GCTACCGTTGAGA	AGGGAAGAAAGGCT	GAGTCTAGGTGG			
B	GGAATTATATTAGT	AGCCGGTGGAGATACA	AGTTCTCTGACTGT	GTGGGAAAGGATAAGT	GCTACCGTTGAGA	AGGGAAGAAAGGCT	GAGTCTAGGTGG			
C	GGAATTATATTAGT	AGCCGGTGGAGATACA	AGTTCTCTGACTGT	GTGGGAAAGGATAAGT	GCTACCGTTGAGA	AGGGAAGAAAGGCT	GAGTCTAGGTGG			
D	GGAATTATATTAGT	AGCCGGTGGAGATACA	AGTTCTCTGACTGT	GTGGGAAAGGATAAGT	GCTACCGTTGAGA	AGGGAAGAAAGGCT	GAGTCTAGGTGG			
E	GGAATTATATTAGT	AGCCGGTGGAGATACA	AGTTCTCTGACTGT	GTGGGAAAGGATAAGT	GCTACCGTTGAGA	AGGGAAGAAAGGCT	GAGTCTAGGTGG			
F	GGAATTATATTAGT	AGCCGGTGGAGATACA	AGTTCTCTGACTGT	GTGGGAAAGGATAAGT	GCTACCGTTGAGA	AGGGAAGAAAGGCT	GAGTCTAGGTGG			

**Fig. 11X-8**



**Fig. 11X-9**



**Fig. 11X-10**

	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100
A	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
B	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
C	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
D	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
E	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
F	GGATTTGAAGTTGAGATCTTTCATCCAAAGAAAGTAGCTTTTCAATTGCTAGAAGCTTAATGTAGCCAAGCCACTTCATTTTTCAGAACTTGTTTACTCATTT									
	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200
A	TATAATATGCGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
B	TATAATATGCGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
C	TATAATATGCGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAATGTTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
D	TATAATATGCGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAATGTTGTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
E	TATAATATGCGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAATGTTGTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
F	TATAATATGCGGAATAAAAAATTTGTGCAAGTCAGAGAAGGGTGCCCTTAAAAATGTTGTGTGGCCAAAGCCACATGAGATCAAAGACACACACTTTTTCATGACCTCA									
	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300
A	AATGTGGGCCCCAGCCTAGGTCAGCCCAACCCCCCATCCAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									
B	AATGTGGGCCCCAGCCTAGGTCAGCCCAACCCCCCATCCAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									
C	AATGTGGGCCCCAGCCTAGGTCAGCCCAACCCCCCATCCAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									
D	AATGTGGGCCCCAGCCTAGGTCAGCCCAACCCCCCATCCAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									
E	AATGTGGGCCCCAGCCTAGGTCAGCCCAACCCCCCATCCAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									
F	AATGTGGGCCCCAGCCTAGGTCAGCCCAACCCCCCATCCAACCCCTTAGACTCACGAACAAATCCACCTGAGATCAGCAGAGCCACCCCTAGATCAGCTGAAACT									

**Fig. 11X-11**

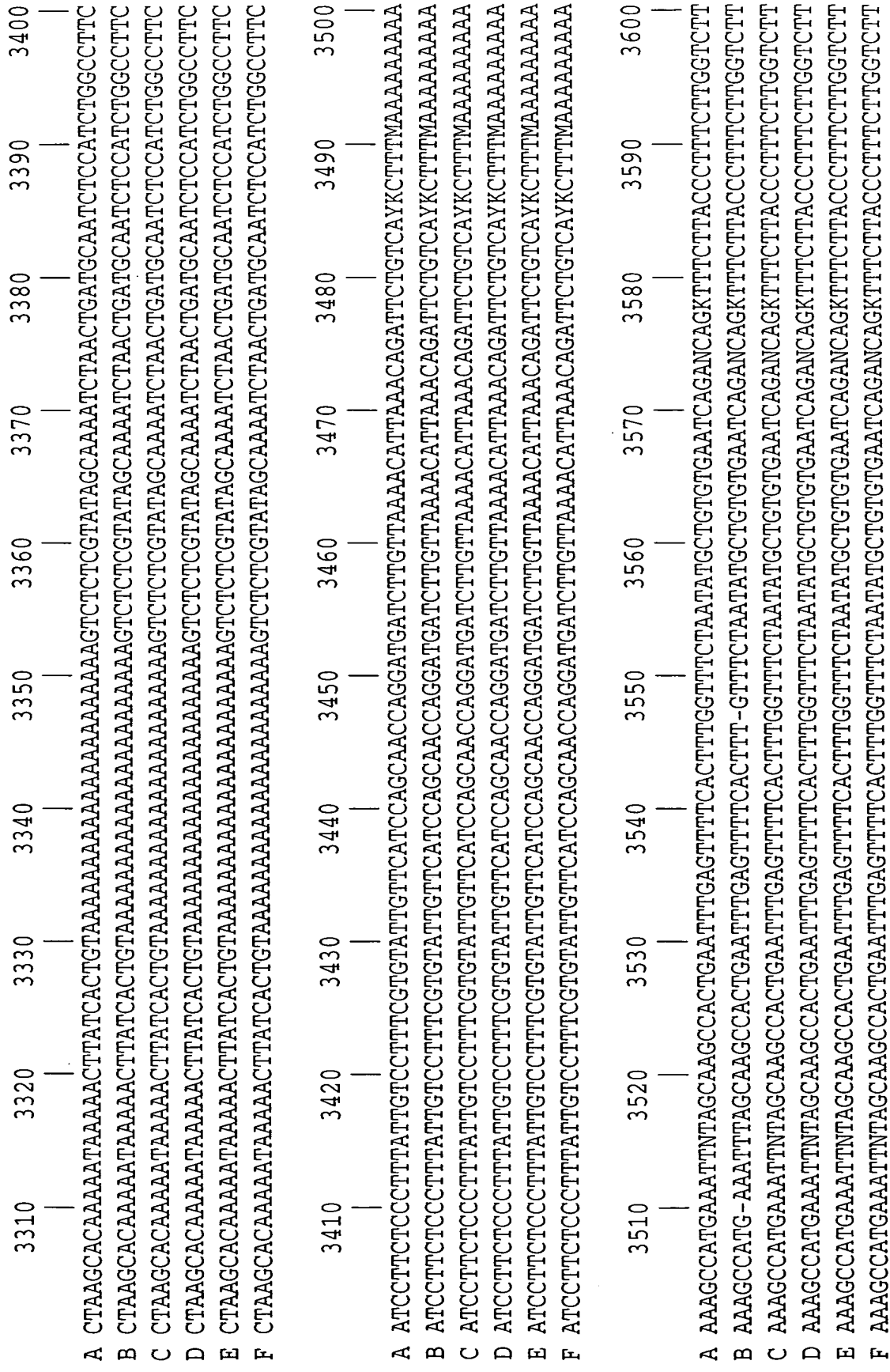


Fig. 11X-12

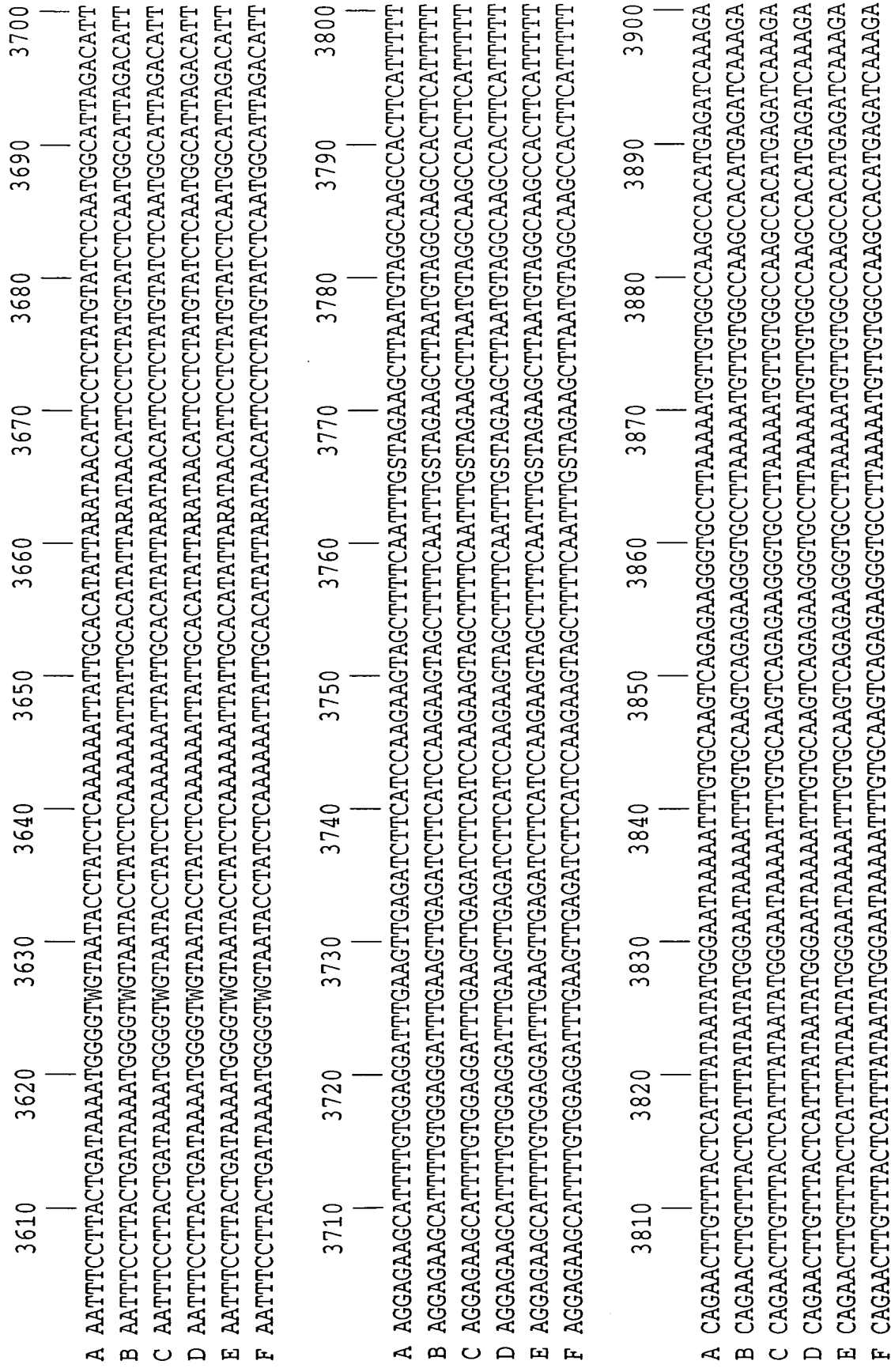


Fig. 11X-13

	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000
A	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGGAACAAATCCACCTGAGATCAGCAGAGCCA									
B	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGGAACAAATCCACCTGAGATCAGCAGAGCCA									
C	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGGAACAAATCCACCTGAGATCAGCAGAGCCA									
D	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGGAACAAATCCACCTGAGATCAGCAGAGCCA									
E	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGGAACAAATCCACCTGAGATCAGCAGAGCCA									
F	CACACTTTTCATGACCTCAAATGTGGGCCCAGCCTAGGTCAGCCAAACCCCATCCAAACCTTAGACTCAGGAACAAATCCACCTGAGATCAGCAGAGCCA									

	4010	4020	4030	4040	4050	4060	4070	4080	4090
A	CCCTAGATCAGCTGAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGAACACCTGCCCGGGCGGCGCGCCC								
B	CCCTAGATCAGCTGAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGAACACCTGCCCGGGCGGCGCGCCC								
C	CCCTAGATCAGCTGAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGAACACCTGCCCGGGCGGCGCGCCC								
D	CCCTAGATCAGCTGAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGAACACCTGCCCGGGCGGCGCGCCC								
E	CCCTAGATCAGCTGAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGAACACCTGCCCGGGCGGCGCGCCC								
F	CCCTAGATCAGCTGAAACTCTAAGCACAAAATAAAAACTTATCACTGTAAAAAATAAAAAAAGAACACCTGCCCGGGCGGCGCGCCC								

**Fig. 11X-14**



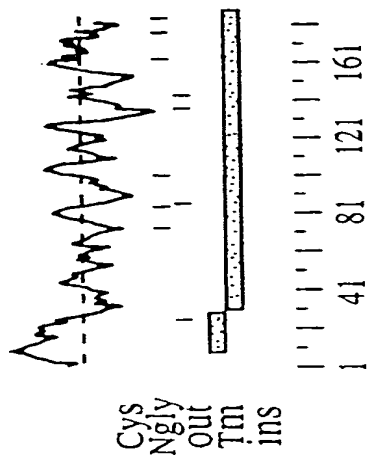


Fig. 11Y-1

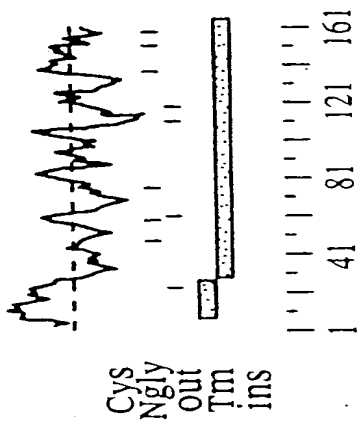


Fig. 11Y-3

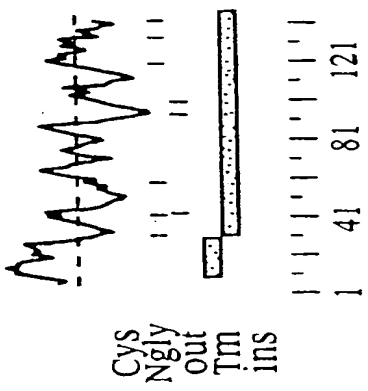


Fig. 11Y-5

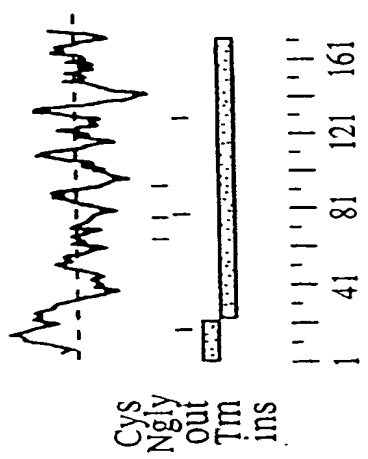


Fig. 11Y-2

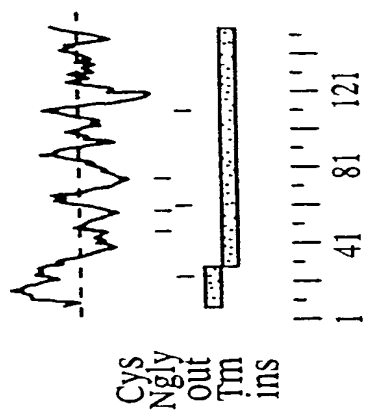


Fig. 11Y-4

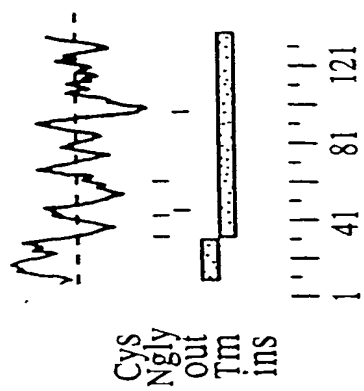


Fig. 11Y-6

GTCGACCCAC	CGGTCCGGTT	TGCTTGGAGA	TGCTGCTAAA	ACAGAGAGGC	TGTGAACAAG	60
GACATTACCG	AGCAGGAGCA	TACATTTCAGA	AGACAAGGAG	CCCTGCTCGC	TGCACCCGAAT	120
ATCTTATCAA	AAAGACTCCT	ATCTGTATGC	CAACCCAGAC	TTCCAGAAAG	AGATCAGATC	180
CCTGAATCCC	CATCATC	ATG AAC	TGG CAC	ATG ATC	ATC TCG GGG CTT ATC	230
	Met Asn	Trp His	Met Ile	Ile Ser	Gly Leu Ile	
	1	5	10			
GTA GTA	GTG ATC	AAA GTT	GTT GGA	ATG ACC	TTT TTT CTG CTG TAT TTC	278
Val Val	Val Ile	Lys Val	Val Val	Gly Met	Thr Phe Phe Leu Leu Tyr Phe	
	15	20	25			
CCA CAG	GTT TTT	GGC AAA	AGT AAT	GAT GGC	TTC GTC CCC ACG GAG AGC	326
Pro Gln	Val Phe	Gly Lys	Ser Ser	Asn Asp	Gly Phe Val Pro Thr Glu Ser	
	30	35	40			
TAC GGA	ACC ACT	AGT GTG	CAG AAT	GTC TCA	CAG ATC TTT GGG AGA AAT	374
Tyr Gly	Thr Thr	Ser Val	Gln Asn	Val Ser	Gln Ile Phe Gly Arg Asn	
	45	50	55			
GAC GAA	AGT ACC	ATG CCT	ACA AGG	AGC TAT	GGA ACA GTC TGT CCC AGA	422
Asp Glu	Ser Thr	Met Pro	Thr Thr	Arg Ser	Tyr Gly Thr Val Cys Pro Arg	
	60	65	70			
AAC TGG	GAT TTT	CAC CAA	GGA AAA	TGC TTT	TTC TTC TCC TTC TCC GAA	470
Asn Trp	Asp Phe	His Gln	Gly Lys	Cys Phe	Phe Ser Phe Ser Glu	
	80	85	90			

**Fig. 11Z-1**

TCA CCT TGG AAA GAC AGC ATG GAT TAT TGT GCA ACA CAA GGA TCC ACA	518
Ser Pro Trp Lys Asp Ser Met Asp Tyr Cys Ala Thr Gln Gly Ser Thr	
95 100 105	
CTG GCA ATT GTC AAC ACT CCA GAG AAA CTG AAG TAT CTT CAG GAC ATA	566
Leu Ala Ile Val Asn Thr Pro Glu Lys Leu Tyr Leu Gln Asp Ile	
110 115 120	
GCT GGT ATT GAG AAT TAC TTT ATT GGT TTG GTA CGT CAG CCT GGA GAG	614
Ala Gly Ile Glu Asn Tyr Phe Ile Gly Leu Val Arg Gln Pro Gly Glu	
125 130 135	
AAA AAG TGG CGC TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC	662
Lys Lys Trp Arg Trp Ile Asn Asn Ser Val Phe Asn Gly Asn Val Thr	
140 145 150 155	
AAT CAG GAC CAG AAC TTC GAC TGT GTC ACT ATA GGT CTG ACG AAG ACA	710
Asn Gln Asp Gln Asn Phe Asp Cys Val Thr Ile Gly Leu Thr Lys Thr	
160 165 170	
TAT GAT GCT GCA TCA TGT GAA GTC AGC TAT CGC TGG ATC TGC GAA ATG	758
Tyr Asp Ala Ala Ser Cys Glu Val Ser Tyr Arg Trp Ile Cys Glu Met	
175 180 185	

**Fig. 11Z-2**

807

AAT GCC AAA TGATCATAGA TCTCTACAAG AGTGAATTTT TACAGAGCTA

Asn Ala Lys

190

867

GCAAAGGAGA TTAGTTGTGA CTGAAACCAG CCCAGGAAAT ATAGAGCATC AAAGACTGTG

927

CCCATCTTCC ATAGGTGGAG TTCCCTATTG AATCCTCAA GTCAATTTGT TACTCCACAA

987

ACATCTTCAC ATAGTAAAC TCCCTTTCTG ACCAAGTATT CCCTAAGACC ACACTTCCTG

1047

TGAGAGGGGA CTGGATTCTA GTTATCTGCA GACAGAGCCA GGATTCTGGA GATGAAATCA

1107

ATATGGAAAT GCAGTCTGTT TCTGTAGAGC TGAGCCTTTTT AACTAATCAG TAGGGTTTTG

1167

TCTGTTGTCA GAACTGTTTG ATCCTTAGAG AACATGCCCA CGCCACTGAG GAGAAACTGC

1227

TCGTGGAACA GATATGAGAA CTGTTAGGAA GCACTATGGG CAGAAGAATA TAAACTTGGC

1287

TTACACAACAT CCCCCATTCC AGAAAGCCTC CCATTCCCAT ACAACATCGT AGAAGCAGAG

1347

GTCCCTTCTGA ATTGGGGAAG GACCTCTACA GCTCGACTTG GTACTGAACA AATATTGAGG

1407

GAATGAAGAA AGTTCTGAAT AGGACAGAGA TAAACAAGGA GGAGAAGGAA AGAGATAGGA

1467

AGAAAGGAGA AGTGGGAAGG AGGGGAAAA GGAATGATGG GCAGGAGAAA AAGAGACAGG

1527

AGCAGCCAGG AAAAACTC AAGCTAAATT TTTTTCAGGT TTTGGATAAA ATCTATTGTG

1587

ACATAAATAA TATCTTTTCA TTAGAAGAGA AAAGGCAAAA TTGGGACAA ATGGGCACCA

1647

TGAGAGATGA AGCAGAGGTT AATTTGATCA CAAGGAAAGA AGGCAGGAA TGAGGTTGAA

1707

AACTTTTGG ATACCTTGGC TGTATCTCA AGAAGGTACA AGCTGCATAA AGTATAGGAG

1767

AAAAGAGATG TGCTGGTTGT TTTAAGTAGC AAAAATTAAA CTACAGAGAA GCCTATAGAA

1827

AGCTAAAGGA ATTAAACCA TCCAATAATC AATTCATTAT TTTCAACTAA TAGCAATATG

1887

TATGTGCATT ACTAGTCAAA ATAAATTGTG AATTCTGTTA TTATAAAAAA AAAAAAAAAG

1896

GGGGCCCGC

Fig. 11Z-3

MI289	ATGAACTGGCACATGATCATCTCGGGGCTTATCGTAGTAGTCAAAAGTTGTTGGAATG	60
HI289	ATGAACTGGCACATGATCATCTCTGGGCTTATTGTGGTAGTGCTTAAAGTTGTTGGAATG	60
MI289	ACCTTTTCTGCTGTATTTCCACAGGTTTGTGGCAAAAGTAATGATGGCTTCGTCCCC	120
HI289	ACCTTATTCTACTTTATTTCACACAGATTTTAAACAAAAGTAACGATGGTTTCACCACC	120
MI289	ACGGAGAGCTACGGAACCACTAGTGTGCAGAAATGTCTCACAGATCTTTGGGAGAGAAATGAC	180
HI289	ACCAGGAGCTATGGAACA-----GTCTCACAGATTTTGGGAGCAGTTCCCCAAGTCCC	174
MI289	GAAAGTACCATGCCACAGGAGCTATGGAACAGTCTGTCCCAAGAACTGGGATTTTCAC	240
HI289	AACGGCTTCATTACCACAGGAGCTATGGAACAGTCTGCCCCCAAAGACTGGGAAATTTTAT	234
MI289	CAAGGAAAATGCTTTTCTTCTCCTTCTCCGAATCACCTTGGAAAGACAGCATGGATTAT	300
HI289	CAAGCAAGATGTTTTTCTTATCCACTCTCTGAATCATCTTGGAATGAAGCAGGGACTTT	294

Fig. 11Z-4

MI289	TGTGCAACACAAGGATCCACACTGGCAATTGTCAACACTCCAGAGAAACTGAAAGTATCTT	360
HI289	TGCAAAAGGAAAAGGATCCACATTTGGCAATTGTCAACACGCCAGAGAAACTGAAAGTTTCTT	354
MI289	CAGGACATAGCTGGTATTGAGAATTACTTTATTGGTTTGGTACGTCAGCCTGGAGAGAAA	420
HI289	CAGGACATAAAGTATGAGAAAGTATTTTATTGGCTTAAATTACCATCGTGAAGAGAGAAA	414
MI289	AAGTGGCGCTGGATCAACAACCTCTGTGTTCATGGCAATGTTACCAATCAGGACCAGAAC	480
HI289	AGGTGGCGTTGGATCAACAACCTCTGTGTTCATGGCAATGTTACATCATCCAATCAGAAT	474
MI289	TTCGACTGTGTCACTATAGGTCTGACGAAGACATATGATGCTGCATCATGTGAAGTCAGC	540
HI289	CAGAAATTCAACTGTGCGACCATTGGCCCTAACAAAGACATTTGATGCTGTGACATCAGC	534
MI289	TATCGCTGGATCTGCGAAATGAATGCCCAA	570
HI289	TACCGCAGGATCTGTGAGAAGAATGCCCAA	564

Fig. 11Z-5

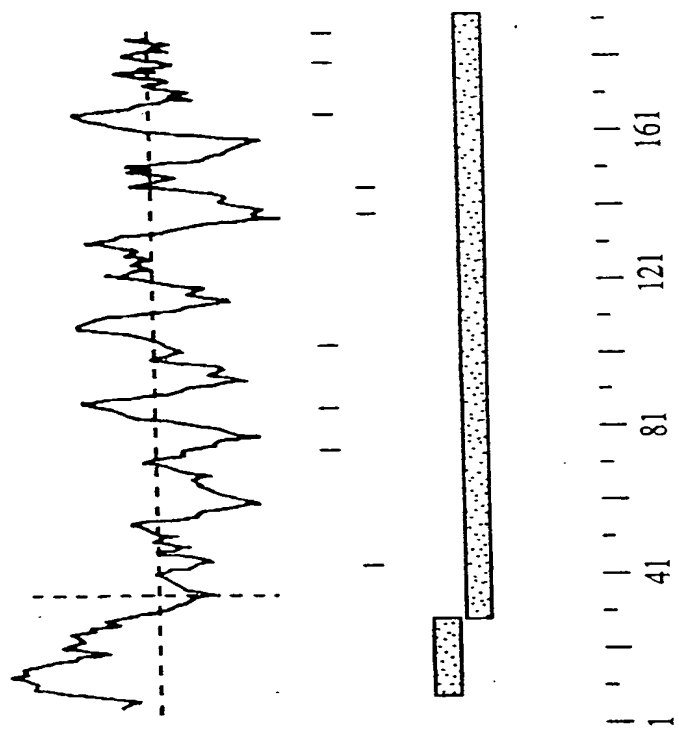


Fig. 11Z-6

L	F	L	G	G	V	G	M	V	G	T	V	A	V	T	V	M	P	Q	19
G	CTG	TTT	CTT	GGT	GGT	GTT	GGA	ATG	GTG	GGC	ACA	GTG	GCT	ACT	GTC	ATG	CCT	CAG	58
W	R	V	S	A	F	I	E	N	N	I	V	V	F	E	N	F	W	E	39
TGG	AGA	GTG	TCG	GCC	TTC	ATT	GAA	AAC	AAC	ATC	ATC	GTT	TTT	GAA	AAC	TTC	TGG	GAA	118
L	W	M	N	C	V	R	Q	A	N	I	R	M	Q	C	K	I	Y	D	59
CTG	TGG	ATG	AAT	TGC	GTG	AGG	CAG	GCT	AAC	ATC	AGG	ATG	CAG	TGC	AAA	ATC	TAT	GAT	178
L	L	A	L	S	P	D	L	Q	A	A	R	G	L	M	C	A	A	S	79
CTG	CTG	GCT	CTT	TCT	CCG	GAC	CTA	CAG	GCA	GCC	AGA	GGA	CTG	ATG	TGT	GCT	GCT	TCC	238
M	S	F	L	A	F	M	M	A	I	L	G	M	K	C	T	R	C	T	99
ATG	TCC	TTC	TTG	GCT	TTC	ATG	ATG	GCC	ATC	CTT	GGC	ATG	AAA	TGC	ACC	AGG	TGC	ACG	298
D	N	E	K	V	K	A	H	I	L	L	T	A	G	I	I	F	I	I	119
GAC	AAT	GAG	AAG	GTG	AAG	GCT	CAC	ATT	CTG	CTG	ACG	GCT	GGA	ATC	ATC	TTC	ATC	ATC	358
G	M	V	V	L	I	P	V	S	W	V	A	N	A	I	I	R	D	F	139
GGC	ATG	GTG	GTG	CTC	ATC	CCT	CTC	AGC	TGG	GTT	GCC	AAT	GCC	ATC	ATC	AGA	GAT	TTC	418
N	S	I	V	N	V	A	Q	K	R	E	L	G	E	A	L	Y	L	G	159
AAC	TCA	ATA	GTG	AAT	GTT	GCC	CAA	AAA	CGT	GAG	CTT	GGA	GAA	GCT	CTC	TAC	TTA	GGA	478

**Fig. 12A**

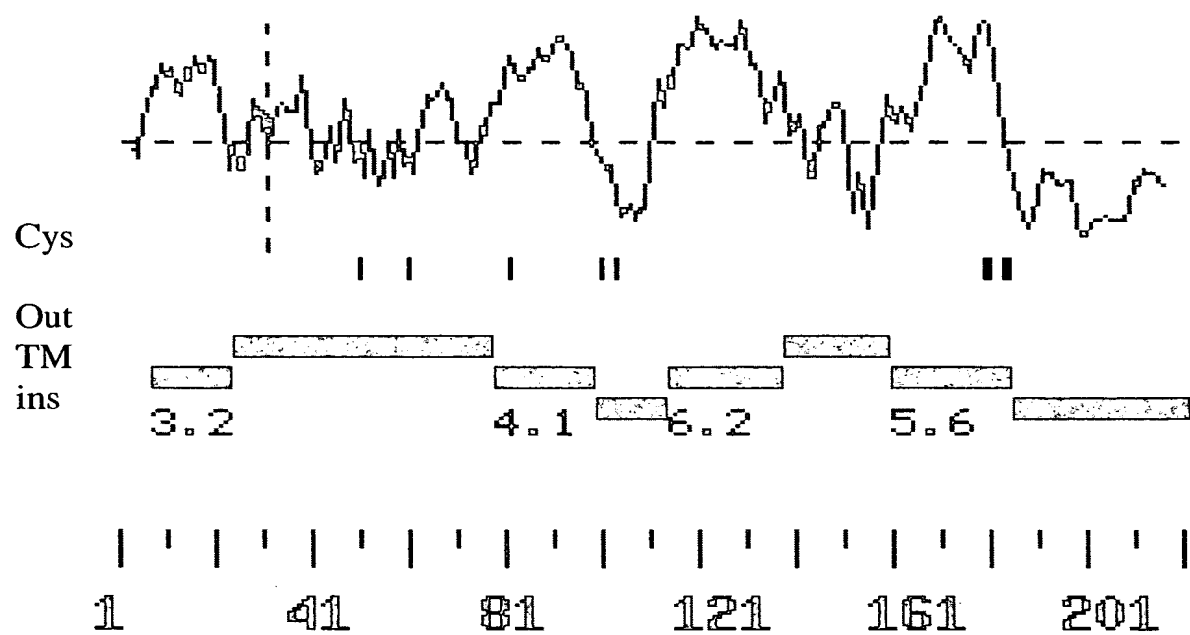


T	A	L	V	L	I	V	G	G	A	L	F	C	C	V	F	C	C	N	179	
ACC	ACG	GCA	CTG	GTG	CTG	ATT	GTT	GGA	GGA	GCT	CTG	TTC	TGC	TGC	GTT	TTT	TGT	TGC	AAC	538
E	K	S	S	S	Y	R	Y	S	I	P	S	H	R	T	T	Q	K	S	Y	199
GAA	AAG	AGC	AGT	AGC	TAC	AGA	TAC	TCG	ATA	CCT	TCC	CAT	CGC	ACA	ACC	CAA	AAA	AGT	TAT	598
H	T	G	K	K	S	P	S	V	Y	S	R	S	Q	Y	V	*				215
CAC	ACC	GGA	AAG	AAG	TCA	CCG	AGC	GTC	TAC	TCC	AGA	AGT	CAG	TAT	GTG	TAG				649
TTGTG	TATG	TTTTTTTAA	CTTTAA	AGCCATG	CAAAATG	ACAAAATC	TATAT	TACTTTCT	CAAAATG	ACCCAA	728									
AGAA	ACTTTG	ATTACTG	TTCTTA	ACTGCC	TAAATCT	TAAATTAC	AGGA	ACTGTG	CATCAG	CTATTTAT	GATTCT	ATAAGC	807							
TATTT	CAGCAG	AATGAG	ATATTA	AAACCA	ATGCTTTG	ATTGTTCT	AGAAA	GTATAG	TAAATTTG	TTTCTA	AGGTG	TTTC	886							
AAG	CACTAC	CTTTTTTAT	CACTTTAC	TTCAAA	ATGACAT	TGCTAA	AGACTG	CATTAT	TTTACT	ACTGTA	ATTTCT	CCAC	965							
GAC	ATAG	CAATAG	ATGATG	AGTAA	CAATTTAT	ATCTCA	CATAG	ACATG	CTTATAT	GTTTAT	TATTTAA	AAATG	1044							
AAATG	CCAG	TCATTA	CACTGA	ATAA	ATAGAA	CTCA	ACTATT	TGCTTT	TCAGG	AAATC	ATGGAT	AGGTTG	AAAGGT	1123						
TACT	ATTA	ATTGTTT	AAAAAC	AGCTTAG	GGATTAA	TGTCCT	CCATTTAT	ATAATG	AAATG	AAATG	AAATG	AAATG	1202							
CATTG	TAAAG	AAATGA	ATGGCTTT	CTGATAT	GCTGTTT	TTAGCC	TAGGAG	TTAGAAA	TCCTA	ACTTCT	TTTATC	CTC	1281							
TTCTC	CCAG	AGGCTTTT	TTTCTT	GTGTAT	TAAATTA	AAACAT	TTTTTA	AAAA	GCAG	ATATTT	TGTCA	AGGGC	TTTG	1360						
TCAAA	CTGCTTT	CCAGG	CTATAC	TCAGAA	GAAAG	ATAAA	AGTGT	GATCTA	AGAAAA	AGTGAT	GGTTT	TAGG	AAAGTG	1439						
AAAA	TATTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	TGTTT	1518						
AGTAT	TTGAG	TACAG	ACTTTG	AGGTTT	TCATCA	ATATA	AAAA	TAAAG	AGCAG	AAAA	TATG	TCTT	GGTTT	1597						

Fig. 12B

CCAAAAACAACAACAAAAAGTTGTCCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCA 1676  
TTTTTGTTCGTGAAAAATAAAATTTCCCTTCTTGTACCAATTTCTGTTTAGTTTTTACTAAAAATCTGTAAATACTGTATTTT 1755  
TCTGTTTATTCCAAAATTTGATGAAACTGACAAATCCAATTTGAAAGTTTGTGTCGACGCTGTCTAGCTTAAATGAATGT 1834  
GTTCTATTTGCTTTATACATTTTATATTAATAAATTGTACATTTTCTAAAAAATAAAAAAATAAAAAAATAAAAAA 1909

**Fig. 12C**



**Fig. 12D**

DKFZ	G-----GGGCA-----
:	: : : :
I309	GCTGTTTCTTGGTGTTGGAATGGTGGGCACACAGTGGCTGTCACTGTCACTGCCTCAGTCGAGAGTGTCG 10      20      30      40      50      60      70
DKFZ	-----
I309	GCCTTCATTGAAAAACAACATCGTGGTTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGCCGTGAGGC 80          90          100        110        120        130        140
DKFZ	-----
I309	AGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTCTGCTGGCTCTTTCTCCGACCTACAGGCAGC 150        160        170        180        190        200        210
DKFZ	-----
I309	CAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCCTTCTTGGCTTTTCATGATGGCCATCCTTGGCATGAAA 220        230        240        250        260        270        280
DKFZ	-----
I309	TGCACCAGGTGCACGGGGACAAATGAGAAGGTGAAGGCTCACATTTCTGTGACGGCTGGAATCATCTTCA 290        300        310        320        330        340        350

**Fig. 12E**

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DKFZ -----
I309 TCATCACGGGCA TGGTGCTCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTTCTATAA
      360      370      380      390      400      410      420
DKFZ -----
I309 CTCAATAGTGAATGTTGCCCCAAAAACGTGAGCTTGGAGAAAGCTCTCTACTTAGGATGGACCACGGCACTG
      430      440      450      460      470      480      490
DKFZ -----
I309 GTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTGCAACGAAAAGACGAGTAGCTACAGAT
      500      510      520      530      540      550      560
DKFZ -----
I309 ACTCGATA CCTTCCCATCGCACAAACCCAAAAAGTTATCACACCCGAAAGAAAGTCACCCGAGCGTCTACTC
      570      580      590      600      610      620      630
DKFZ -----
I309 CAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTTAACTTTACTATAAAGCCAATGCAAAATGACAAAAATC
      640      650      660      670      680      690      700

```

**Fig. 12F**

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DKFZ -----
I309 TATATTACTTCTCAAAATGGACCCCAAGAAACTTTGATTACTGTCTTAACCTGCCCTAAATCTTAATTA
      710      720      730      740      750      760      770

DKFZ -----
I309 CAGGAACTGTGCATCAGCTATTTATGATTCTATAAGCTATTTTCAGCAGAAATGAGATATATAACCCCAATGC
      780      790      800      810      820      830      840

      30      40      50      60      70      80      90
DKFZ TTTGATTGTTCTAGAAAGTATAGTAATTTGTTTCTAAGGTGGTTCAAGCATCTACTCTTTTATCATTT
      :      :      :      :      :      :      :      :      :      :      :      :
I309 TTTGATTGTTCTAGAAAGTATAGTAATTTGTTTCTAAGGTGGTTCAAGCATCTACTCTTTTATCATTT
      850      860      870      880      890      900      910

      100     110     120     130     140     150     160
DKFZ ACTTCAAAATGACATTGCTAAAGACTGCAATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGT
      :      :      :      :      :      :      :      :      :      :      :      :
I309 ACTTCAAAATGACATTGCTAAAGACTGCAATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGT
      920     930     940     950     960     970     980

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**Fig. 12G**

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170      180      190      200      210      220      230
DKFZ ACATAGATGAGTGTAACATTATATCTCACATAGAGACATGCTTATATGGTTTTATTATAAAATGAAATGC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 ACATAGATGAGTGTAACATTATATCTCACATAGAGACATGCTTATATGGTTTTATTATAAAATGAAATGC
      990      1000      1010      1020      1030      1040      1050

240      250      260      270      280      290      300
DKFZ CAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGGAAATCATGGATAGGGTTGAAGAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 CAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGGAAATCATGGATAGGGTTGAAGAA
      1060      1070      1080      1090      1100      1110      1120

310      320      330      340      350      360      370
DKFZ GGTACTATTAAATGTTTTTAAAAACAGCTTAGGGATTAATGTCCCTCCATTATATAATGAAGATTAAAAATGA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 GGTACTATTAAATGTTT-AAAAACAGCTTAGGGATTAATGTCCCTCCATTATATAATGAAGATTAAAAATGA
      1130      1140      1150      1160      1170      1180

380      390      400      410      420      430      440
DKFZ AGGCTTTAATCAGCATTTGTAAAGGAAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
I309 AGGCTTTAATCAGCATTTGTAAAGGAAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAG
      1190      1200      1210      1220      1230      1240      1250

```

**Fig. 12H**

450	460	470	480	490	500	510
DKFZ	AAATCCTAACTTCTTTATCCTCTTCTCTCCAGAGGCTTTT	TTTTTCTTCTTG	TATTA	AAATTAACATTTT	TAA	
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
I309	AAATCCTAACTTCTTTATCCTCTTCTCTCCAGAGGCTTTT	TTTTTCTTCTTG	TATTA	AAATTAACATTTT	TAA	
1260	1270	1280	1290	1300	1310	1320
520	530	540	550	560	570	580
DKFZ	AAAGCAGATATTTTGTCAAGGGGCTTTTGCAATTC	AAACTGCTTTTCCAGGGCTATACTCAGAAAG	AAGATA			
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
I309	AAAGCAGATATTTTGTCAAGGGGCTTTTGCAATTC	AAACTGCTTTTCCAGGGCTATACTCAGAAAG	AAGATA			
1330	1340	1350	1360	1370	1380	1390
590	600	610	620	630	640	650
DKFZ	AAAGTGTGATCTAAGAAAAAGTGATGGTTTTTAGGAAAGT	GAAAAATATTTT	TGTTTGTATTTGAAGAAG			
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
I309	AAAGTGTGATCTAAGAAAAAGTGATGGTTTTTAGGAAAGT	GAAAAATATTTT	TGTTTGTATTTGAAGAAG			
1400	1410	1420	1430	1440	1450	1460
660	670	680	690	700	710	720
DKFZ	AATGATGCATTTTGACAAGAAATCATATATGTATGGATATA	TTTAAATAAGTATTTGAGTACAGACTTTG				
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
I309	AATGATGCATTTTGACAAGAAATCATATATGTATGGATATA	TTTAAATAAGTATTTGAGTACAGACTTTG				
1470	1480	1490	1500	1510	1520	1530

**Fig. 12I**



730	740	750	760	770	780	790
DKFZ	AGGTTTCATCAATATAATAAAGAGCAGAAAAATATGTCCTTGGTTTTCATTTGCTTACCACAAAAACAA					
	::					
I309	AGGTTTCATCAATATAATAAAGAGCAGAAAAATATGTCCTTGGTTTTCATTTGCTTACCACAAAAACAA					
1540	1550	1560	1570	1580	1590	1600
800	810	820	830	840	850	860
DKFZ	CAACAAAAAAGTTGTCCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAAATTGTCATTT					
	::					
I309	CAACAAAAAAGTTGTCCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAAATTGTCATTT					
1610	1620	1630	1640	1650	1660	1670
870	880	890	900	910	920	930
DKFZ	TTGTTCTGTGAAAAATAAAATTTCCCTTCTTGTAACCATTTCTGTTAGTTTACTAAAAATCTGTAAATACTG					
	::					
I309	TTGTTCTGTGAAAAATAAAATTTCCCTTCTTGTAACCATTTCTGTTAGTTTACTAAAAATCTGTAAATACTG					
1680	1690	1700	1710	1720	1730	1740
940	950	960	970	980	990	1000
DKFZ	TATTTTCTGTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCGTCT					
	::					
I309	TATTTTCTGTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCGTCT					
1750	1760	1770	1780	1790	1800	1810

**Fig. 12J**

1010	1020	1030	1040	1050	1060	1070
DKFZ	AGCTTAAATGAATGTTCTATT	TGCTTTATACATTATTAATAA	TTGTACATTTT	TCCAAAAAAA		
	::::::::::::::::::::::::::::	::::::::::::::::::::::::::::	::::::::::::::::::::::::::::	::::::::::::::::::::::::::::		
I309	AGCTTAAATGAATGTTCTATT	TGCTTTATACATTATTAATAA	TTGTACATTTT	TCTAAAAAAA		
1820	1830	1840	1850	1860	1870	1880
1080	1090					
DKFZ	AAAAAAA	-----				
	::::::::::::					
I309	AAAAAAA	AAAAAAA				
1890	1900					

**Fig. 12K**

I309	G-----CTGTTTCTTGGTGTGGAATGGTGGGCACAGTGGCTG	10	20	30	40	50	60	70
CLAUD8	ATGGCAACCTACGCTCTTCAAATGGCTGCACTGGTGTGTTGGCATGGTGGGCACGGTGGCTG	10	20	30	40	50	60	70
I309	TCACCTGTCAATGCCTCAGTGGAGAGTGTGGCCCTTCATTGAAAAACAACATCGTGGTTTTGTGAAAACTTCTG	50	60	70	80	90	100	110
CLAUD8	TGACTATCATGCTCAGTGGAGAGTGTCTGCCCTTCATCGAAAAGTAACATTTGGTGTTTTGAGAACCGCTG	80	90	100	110	120	130	140
I309	GGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTG	120	130	140	150	160	170	180
CLAUD8	GGAAGGCTTGTGGATGAATTGTATGAGGCATGCCAACATCAGAATGCAGTGCAAGGTCTACGACTCCCTG	150	160	170	180	190	200	210
I309	CTGGCTCTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCCTTCTTTG	190	200	210	220	230	240	250
CLAUD8	CTGGCTCTTAGTCCAGACCTCCAGGCATCCCGAGGACTGATGTGTGCTGCGTCCGCTTGGCTTTCTTTG	220	230	240	250	260	270	280

**Fig. 12L**

I309	CTTTCATGATGCCCATCCTTGGCATGAAATGCACACAGGTGCACGGGGACAAATGAGAAGGTGAAGGCTCA	260	270	280	290	300	310	320
CLAUD8	CTTTCATGACAGCCATCCTCGGAATGAAGTGCACACAGATGCACGGGGACGATGAGAACCTGAAGAGCCG	290	300	310	320	330	340	350
I309	CATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCATCCCTGTGAGCTGGGTT	330	340	350	360	370	380	390
CLAUD8	CATCTTGCTGACAGCCGGAATCATCTTCTTCATCACCGGCTTGGTTGTGCTCATCCCTGTGAGCTGGGTT	360	370	380	390	400	410	420
I309	GCCAAATGCCCATCATCAGAGATTTCATAACTCAATAGTGAATGTTGCCCAAAACGTGAGCTTGGAGAAG	400	410	420	430	440	450	460
CLAUD8	GCCAAATTCATCATCAGAGACTTCTACAACCCACTGGTGGATGTGGCCCTAAAGCCGAGCTGGGAGAAG	430	440	450	460	470	480	490
I309	CTCTCTACTTAGGATGGACCACGGCAGCTGGTGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTG	470	480	490	500	510	520	530
CLAUD8	CCCTCTACATAGGCTGGACCACAGCGCTGGTGTGATCGCTGGAGGAGCACTGTTCTGTGTGTTTTTG	500	510	520	530	540	550	560

**Fig. 12M**

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540      550      560      570      580      590      600
I309 TTGCAACGAAAGAGCAGTAGCTACAGATACTCGATACCTTCCCATCGCACAAACCCAAAAAGTTATCAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAUD8 TTGTACTGAAAGGAGCAACAGTTACAGGTACTCGGTACCATCCCATCGCACCACTCAACGGAGTTTCCAC
      570      580      590      600      610      620      630

      610      620      630      640      650      660      670
I309 ACCGGAAAGAGTCACCGAGCGTCTACTCCAGAAGTCAAGTATGTGTAGTTGTGTATGTTTTTAACTTT
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
CLAUD8 GCCGAAAAGAGATCTCCGAGCATATATACTCCAAAAGTCAGTATGTGTAG-----
      640      650      660      670

      680      690      700      710      720      730      740
I309 ACTATAAGCCATGCAAATGACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAAACTTTGATT
CLAUD8 -----

      750      760      770      780      790      800      810
I309 TACTGTTCTTAACTGCCCTAATCTTAATTACAGGAACGTGTCATCAGCTATTTATGATTCCTATAAGCTATT
CLAUD8 -----

```

**Fig. 12N**

	820	830	840	850	860	870	880
I309	TCAGCAGAA	TGAGATAT	TAAACCA	TGCTT	TGATT	GTTCTAG	AAAGTATAGTA
							ATTTGTTTTTCTAAGGT
CLAUD8	-----						
	890	900	910	920	930	940	950
I309	GGTTCAAG	CATCTCT	TTTTTAT	CATTACT	TCAAAAT	GCATTG	CTAAAGACTGCAT
							TATTTTACTAC
CLAUD8	-----						
	960	970	980	990	1000	1010	1020
I309	TGTAATT	TCTCCAC	GACATAG	CATTATG	TACATAG	ATGAGTG	TAAACATTTAT
							TATCTCACATAGAGACATG
CLAUD8	-----						
	1030	1040	1050	1060	1070	1080	1090
I309	CTTATAT	GGTTTT	TATTTAA	AAATGAA	ATGCCAG	TCCATTAC	ACTGAATAAGAACT
							CAACTATTGCTTT
CLAUD8	-----						
	1100	1110	1120	1130	1140	1150	1160
I309	TCAGGAA	AATCATG	GATAGG	GTGAAG	AAGGTTA	CTACTAT	TAAATGTTTAAAA
							ACAGCTTAGGGATTAAATGT
CLAUD8	-----						

Fig. 120

	1170	1180	1190	1200	1210	1220	1230
I309	CCTCCATTTATAATGAAGATTAAATGAAGCTTTAATCAGCATTTGTAAAGGAAATTGAAATGGCTTTCTG						
CLAUD8	-----						
	1240	1250	1260	1270	1280	1290	1300
I309	ATATGCTGTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTT						
CLAUD8	-----						
	1310	1320	1330	1340	1350	1360	1370
I309	TTCTTGTTGTTAAATTAACATTTTTTAAAAAGCAGATATTTTGTCAAGGGGCTTGCATTCAAACCTGCTT						
CLAUD8	-----						
	1380	1390	1400	1410	1420	1430	1440
I309	TTCCAGGGCTATACTCAGAAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGAA						
CLAUD8	-----						

**Fig. 12P**

	1450	1460	1470	1480	1490	1500	1510
I309	AATATTTTGTGTAATTTGAAGAAGAAATGATGCATTTTGGACAAGAAATCATATATGTATGGATATAT						
CLAUD8	-----						
	1520	1530	1540	1550	1560	1570	1580
I309	TTTAAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAGAGCAGAAAAATATGTCTT						
CLAUD8	-----						
	1590	1600	1610	1620	1630	1640	1650
I309	GGTTTTCATTTGCTTACCATAAAACAAACAAAAAGTTGTCTTTGAGAACTTCACCTGCTCCTAT						
CLAUD8	-----						
	1660	1670	1680	1690	1700	1710	1720
I309	GTGGGTACCTGAGTCAAAATTGTCAATTTTGTCTGTGAAAAATAAATTCCTTCTTGTAACCATTTCTGT						
CLAUD8	-----						
	1730	1740	1750	1760	1770	1780	1790
I309	TTAGTTTACTAAAAATCTGTAAATACTGTATTTTCTGTATTATTCCAAATTTGATGAAACTGACAATCCA						
CLAUD8	-----						

**Fig. 12Q**



	1800	1810	1820	1830	1840	1850	1860
I 309	ATTGAAAGTTTGTGTCGACGCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATATT						
CLAUD8	-----						
I 309	AATAAATTGTACATTTTCTAAAAAATAAAAAAATAAAAAA						
CLAUD8	-----						

**Fig. 12R**

	10	20	30	40	50	60	70
CLAUD8	MATYALQMAALVLGGVGMVGTVAVTIMPQWRVSAFIESNIVVFENRWEGLWMNCMRHANIRMQCKVYDSL						
	:	:	:	:	:	:	:
I309	-----LFLGGVGMVGTVAVTMPQWRVSAFIENNIVVFENFWEGLMNCVRQANIRMQCKIYDSL	10	20	30	40	50	60
	80	90	100	110	120	130	140
CLAUD8	LALSPDLQASRGLMCAASVLAFLAFMTAILGMKCTRCTGDDENVKSRILLTAGIIFFITGLVVLIPVSWV						
	:	:	:	:	:	:	:
I309	LALSPDLQAARGLMCAASVMSFLAFMTAILGMKCTRCTGDNEKVKAHILLTAGIIFIITGMVVLIPVSWV	70	80	90	100	110	120
							130
	150	160	170	180	190	200	210
CLAUD8	ANSIIRDFYNPLVDVALKRELGEALYIGWTTALVLIAGGALFCCVFCCTERSNSYRYSVPSHRTTQRSFH						
	:	:	:	:	:	:	:
I309	ANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCKNEKSSSYRYSIPSHRTTQKSYH	140	150	160	170	180	190
							200
	220						
CLAUD8	AEKRSPSIYSKSQYV						
	.	:	:	:	:	:	:
I309	TGKKSPSVYSRSQYV						
							210

**Fig. 12S**

I309 .....LFLGGVGMVGTVAVTMPQWRVSAFIENNIVVFENFWEGL 40  
 hCPE MASMGLQVMGIALAVLGLWLAVMLCCALPMWRVTAFIGSNIIVTSQTIWEGL 50  
 mCPE MASMGLQVLGISLAVLGLWLGIIILSCALPMWRVTAFIGSNIIVTAQTSWEGL 50  
 rRPV .MSMSLEITGTSLAVLGLWNLCTIVCCALPMWRVSAFIGSSIIITAQITWEGL 49  
  
 I309 WMNCVRQANIRMQCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAIL 90  
 hCPE WMNCVVQSTGMQCKVYDSLALPQDLQAARALVISIIVAALGVLLSVV 100  
 mCPE WMNCVVQSTGMQCKMYDSMLALPQDLQAARALMVISIIVGALGMLLSVV 100  
 rRPV WMNCV.QSTGMQCKMYDSLALPQDLQAARALIVVSILLAAFGLLVALV 98  
  
 I309 GMKCTRCTGDNEKVKAHILLTAGIIFIITGMVVLIPVSWVANAIIRDFYN 140  
 hCPE GGKCTNCLED.ESAKAKTMIVAGVVFLLAGLMVIVPVSWTAHNI IQDFYN 149  
 mCPE GGKCTNCMED.ETVKAKIMITAGAVFIVASMLIMVPVSWTAHNVIRDFYN 149  
 rRPV GAQCTNCVQD.ETAKAKITIVAGVLFLLAAVLTLVPVSWSANTIIRDFYN 147  
  
 I309 SIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVCCNEKSSSYRYSIP 190  
 hCPE PLVASGQKREMGASLYVGWAAAGLLLLGGGLCC.NCPRTDKPYSAKYS 198  
 mCPE PMVASGQKREMGASLYVGWAAAGLLLLGGGLCCSCPPRNDKPYSAKYS 199  
 rRPV PLVPEAQKREMGTGLYVGWAAAALQLLGGALLCCSCPPREKYAPTILYS 197  
  
 I309 SHRTTQKSYHTGKKSPSVYSRSQYV 215  
 hCPE AARSAASNYV..... 209  
 mCPE AARSVPASNYV..... 210  
 rRPV APRSTGPGTGTAYDRKTTSERPGARTPHHHYQPSMYPTRPACSLASET 248

**Fig. 12T**

CGAGCGGCGCGCGG	CAGGTCAGACATGGGCCAAGGAGCCAGAGCCGTCGCGGGTCTGTGAGTTGAGCTTGAGGCCG	79																		
M	R	V	I	M	G	I	A	S	L	G	F	L	W	A	V	F	L	18		
CAGG	ATG	AGG	GTC	ATC	ATG	GGG	ATA	GCC	AGC	CTG	GGG	TTC	CTC	TGG	GCA	GTA	TTC	CTG	137	
L	P	L	V	F	G	V	P	T	E	E	T	T	F	G	E	S	V	A	S	38
CTT	CCT	CTT	GTG	TTT	GGG	GTC	CCC	ACA	GAG	GAG	ACT	ACC	TTT	GGA	GAA	TCT	GTG	GCC	TCC	197
H	L	P	K	G	C	R	R	C	C	D	P	E	D	L	M	S	S	D	D	58
CAT	CTC	CCC	AAA	GGC	TGT	CGA	CGA	TGC	TGT	GAC	CCC	GAG	GAC	CTG	ATG	TCC	TCT	GAT	GAT	257
T	V	Q	A	P	V	S	P	Y	V	L	P	E	V	R	P	Y	L	G	R	78
ACG	GTC	CAG	GCC	CCT	GTT	TCC	CCT	TAT	GTC	CTG	CCT	GAA	GTC	AGG	CCG	TAC	CTC	GGC	CGC	317
D	H																		80	
GAC	CAC																			323

Fig. 13A

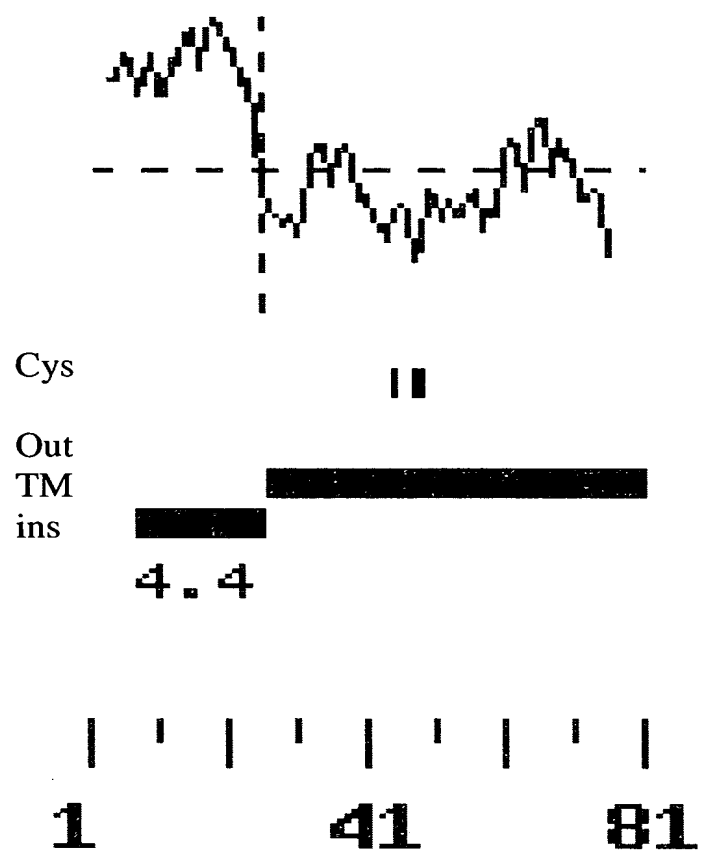
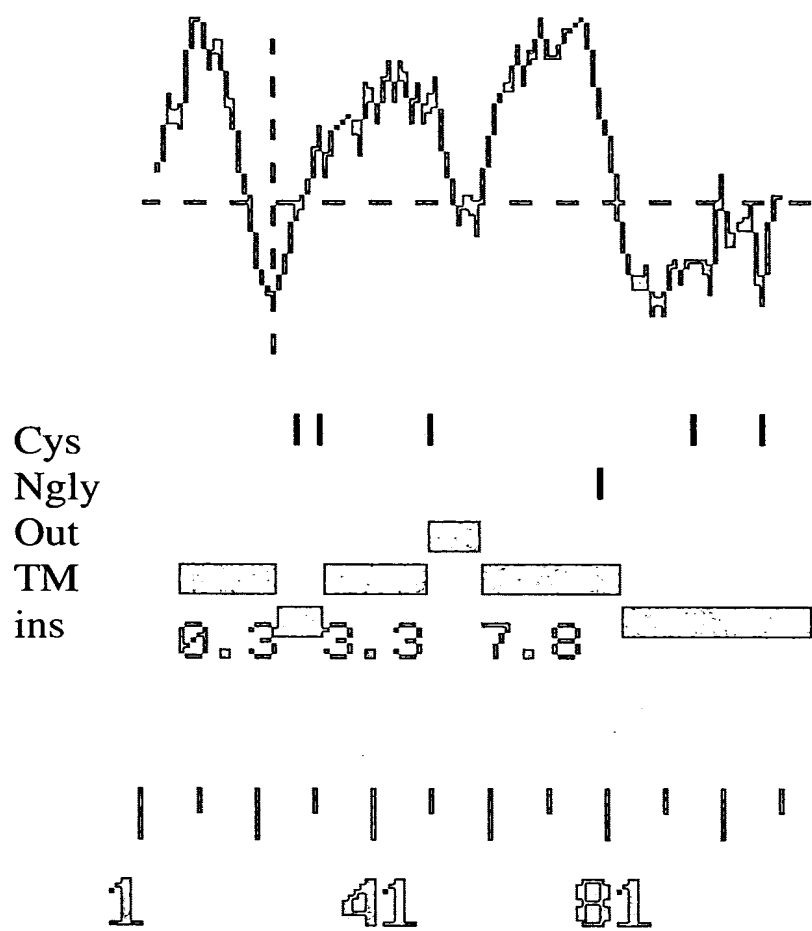


Fig. 13B

CGGACGCGTGGCGGACGCGTGGGTTATTCTTTGGTTGTAGGTATAAATATGGCATTTAAAAACAACACCCAGTTT	79
M      E      F      L      Y      R      I      V      V      G      F      I      L      I      F      T	16
TGTACTIONAAGT ATG GAA TTC TTA TAT AGG ATT GTT GGT GGA TTC ATT CTT ATC TTT ACA	142
F      F      N      I      K      G      Q      N      T      K      C      P      M      S      C      Y      Y      I      V      R	36
TTT TTT AAT ATT AAG GGA CAG AAT ACC AAG TGT CCA ATG TCT TGT TAT TAT ATT GTT AGG	202
V      L      G      T      L      G      I      L      T      V      F      W      V      C      P      L      T      I      F      N	56
GTA CTG GGC ACT TTG GGG ATA TTG ACT GTA TTC TGG GTT TGC CCC CTC ACT ATT TTT AAT	262
P      D      Y      F      I      P      I      S      I      T      I      V      L      T      L      L      G      I      L	76
CCA GAC TAT TTT ATA CCT ATC AGT ATA ACT ATA GTT CTT ACT CTT CTT CTT GGA ATT CTT	322
F      L      I      V      Y      Y      G      S      F      H      P      N      R      S      A      E      T      K      C      D	96
TTT CTT ATT GTT TAT TAT GGG AGT TTT CAC CCA AAC AGA AGT GCA GAA ACA AAA TGT GAT	382
E      I      D      G      K      P      V      L      R      E      C      R      M      R      Y      F      L      M      E      *	115
GAA ATT GAT GGA AAA CCA GTT CTA AGA GAA TGT AGA ATG AGA TAT TTC CTA ATG GAA TAA	442
GCTATTCATTTATGATATATATTTTCTTATATTTTGTTCATTGGTTAGTAAAGAAATGTGTGTAAATAAAAAAAAAA	521
AAAAAAAAAAAAAAAAAAAAAAAAA	546

Fig. 14A



**Fig. 14B**

CGGACGCGGTGGCGGACGCGTGGCAGCTGAAGAAAGAGAGGA	ATG	AAG	CGC	CTT	CTG	CTT	CTG	CTT	CTG	TTT	8									
L	F	F	I	T	F	S	A	F	P	L	V	R	M	T	E	N	E	E	28	
TTG	TTC	TTT	ATA	ACA	TTT	TCT	TCT	GCA	TTT	CCC	TTA	GTC	CGG	ATG	ACG	GAA	AAT	GAA	GAA	128
N	M	Q	L	A	Q	A	Y	L	N	Q	F	Y	S	L	E	I	E	G	N	48
AAT	ATG	CAA	CTG	GCT	CAG	GCA	TAT	CTC	AAC	CAG	TTC	TAC	TCT	CTT	GAA	ATA	GAA	GGG	AAT	188
H	L	V	Q	S	K	N	R	S	L	I	D	D	K	I	R	E	M	Q	A	68
CAT	CTT	GTT	CAA	AGC	AAG	AAT	AGG	AGT	CTC	ATA	GAT	GAC	AAA	ATT	CGG	GAA	ATG	CAA	GCA	248
F	F	G	L	T	V	T	G	K	L	D	S	N	T	L	E	I	M	K	T	88
TTT	TTT	GGA	TTG	ACA	GTG	ACT	GGA	AAA	CTG	GAC	TCA	AAC	ACC	CTT	GAG	ATC	ATG	AAG	ACA	308
P	R	C	G	V	P	D	V	G	Q	Y	G	Y	T	L	P	G	W	R	K	108
CCC	AGG	TGT	GGG	GTG	CCT	GAT	GTG	GGC	CAG	TAT	GGC	TAC	ACC	CTC	CCT	GGG	TGG	AGA	AAA	368
Y	N	L	T	Y	R	I	I	N	Y	T	P	D	M	A	R	A	A	V	D	128
TAC	AAC	CTC	ACC	TAC	AGA	ATA	ATA	AAC	TAT	ACT	CCG	GAT	ATG	GCA	CGA	GCT	GCT	GTG	GAT	428
E	A	I	Q	E	G	L	E	V	W	S	K	V	T	P	L	K	F	T	K	148
GAG	GCT	ATC	CAA	GAA	GGT	TTA	GAA	GTG	TGG	AGC	AAA	GTC	ACT	CCA	CTA	AAA	TTC	ACC	AAG	488

**Fig. 15A**



I S K G I A D I M I A F R T R V H G R C	168
ATT TCA AAG GGG ATT GCA GAC ATC ATG ATG ATT GCC TTT AGG ACT CGA GTC CAT GGT CGG TGT	548
P R Y F D G G P L G V L G H A F P P G P G	188
CCT CGC TAT TTT GAT GGT CCC TTG GGA GTG GTG CTT GGC CAT GCC TTT CCT CCT GGT CCG GGT	608
L G G D T H F D E D E N W T K D G A G F	208
CTG GGT GGT GAC ACT CAT TTT GAT GAG GAT GAA AAC TGG ACC AAG GAT GGA GCA GGA TTC	668
N L F L V A A H E F G H A L G L S H S N	228
AAC TTG TTT CTT GTG GCT GCT CAT GAA TTT GGT CAT GCA CTG GGC CTC TCT CAC TCC AAT	728
D Q T A L M F P N Y V S L D P R K Y P L	248
GAT CAA ACA GCC TTG ATG TTC CCA AAT TAT GTC TCC CTG GAT CCC AGA AAA TAC CCA CTT	788
S Q D D I N G I Q S I Y G G L P K V P A	268
TCT CAG GAT GAT ATC AAT GGA ATC CAG TCC ATC TAT GGA GGT CTG CCT AAG GTA CCT GCT	848
K P K E P T I P H A C D P D L L T F D A I	288
AAG CCA AAG GAA CCC ACT ATA CCC CAT GCC TGT GAC CCT GAC TTG ACT TTT GAC GCT ATC	908
T T F R R E V M F F K G R H L L W R I Y Y	308
ACA ACT TTC CGC AGA GAA GTA ATG TTC TTT AAA GGC AGG CAC CTA TGG AGG ATC TAT TAT	968

**Fig. 15B**

D	I	T	D	V	E	F	E	L	I	A	S	F	W	P	S	L	P	A	D	328
GAT	ATC	ACG	GAT	GTT	GAG	TTT	GAA	TTA	ATT	GCT	TCA	TTT	TGG	CCA	TCT	CTG	CCA	GCT	GAT	1028
L	Q	A	A	Y	E	N	P	R	D	K	I	L	V	F	K	D	E	N	F	348
CTG	CAA	GCT	GCA	TAC	GAG	AAC	CCC	AGA	GAT	AAG	ATT	CTG	GTT	TTT	AAA	GAT	GAA	AAC	TTC	1088
W	M	I	R	G	Y	A	V	L	P	D	Y	P	K	S	I	H	T	L	G	368
TGG	ATG	ATC	AGA	GGA	TAT	GCT	GTC	TTG	CCA	GAT	TAT	CCC	AAA	TCC	ATC	CAT	ACA	TTA	GGT	1148
F	P	G	R	V	K	K	I	D	A	A	V	C	D	K	T	T	R	K	T	388
TTT	CCA	GGA	CGT	GTG	AAG	AAA	ATA	GAT	GCA	GCC	GTC	TGT	GAT	AAG	ACC	ACA	AGA	AAA	ACC	1208
Y	F	F	V	G	I	W	C	W	R	F	D	E	M	T	Q	T	M	D	K	408
TAC	TTC	TTT	GTG	GGC	ATT	TGG	TGC	TGG	AGG	TTT	GAT	GAA	ATG	ACC	CAA	ACC	ATG	GAC	AAA	1268
G	F	P	Q	R	V	V	K	H	F	P	G	I	S	I	R	V	D	A	A	428
GGA	TTC	CCG	CAG	AGA	GTG	GTA	AAA	CAC	TTT	CCT	GGA	ATC	AGT	ATC	CGT	GTT	GAT	GCT	GCT	1328
F	Q	Y	K	G	F	F	F	F	S	R	G	S	K	Q	F	E	Y	N	I	448
TTC	CAG	TAC	AAA	GGA	TTC	TTT	TTT	TTC	AGC	CGT	GGA	TCA	AAG	CAA	TTT	GAA	TAC	AAC	ATT	1388
K	T	K	N	I	T	R	I	M	R	T	N	T	W	F	Q	C	K	E	P	468
AAG	ACA	AAG	AAT	ATT	ACC	CGA	ATC	ATG	AGA	ACT	AAT	ACT	TGG	TTT	CAA	TGC	AAA	GAA	CCA	1448

Fig. 15C

K	N	S	S	F	G	F	D	I	N	K	E	K	A	H	S	G	G	I	K	488																		
AAG	AAC	TCC	TCA	TTT	GGT	TTT	GAT	ATC	AAC	AAG	GAA	AAA	GCA	CAT	TCA	GGA	GGC	ATA	AAG	1508																		
I	L	Y	H	K	S	L	S	L	F	I	F	G	I	V	H	L	L	K	N	508																		
ATA	TTG	TAT	CAT	AAG	AGT	TTA	AGC	TTG	TTT	ATT	TTT	GGT	ATT	GTT	CAT	TTG	CTG	AAA	AAC	1568																		
T	S	I	Y	Q	*															514																		
ACT	TCT	ATT	TAT	CAA	TAA															1586																		
ATT																				CAT	AGACCT	AAAT	AAACCT	CAACAGG	CTTT	TTAATA	TAAAT	TCTGCT	TCAA	AAAT	AGAA	TAAAA	CCATT	CTTT	AAC	1665		
AAC																				AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	1684

Fig. 15D

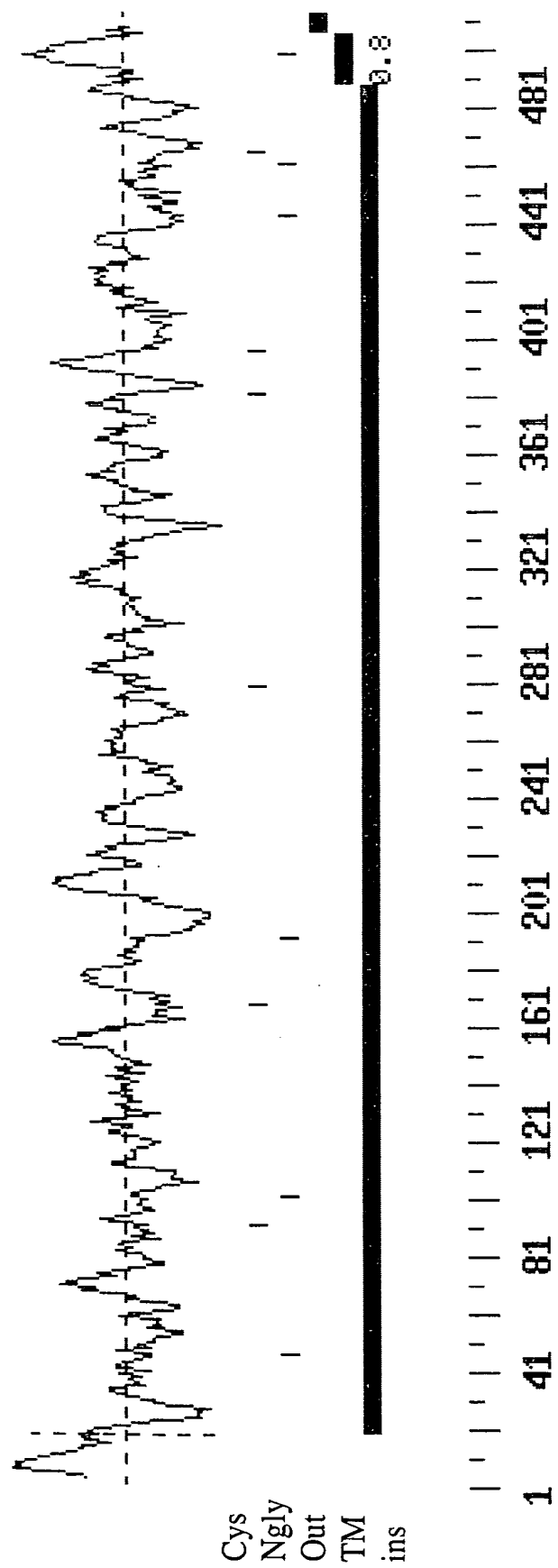


Fig. 15E



A	D	I	M	I	A	F	R	T	G	V	H	G	W	C	P	R	H	F	D	173
GCA	GAT	ATA	ATG	ATA	GCA	TTC	AGG	ACA	GGA	GTC	CAT	GGC	TGG	TGT	CCT	CGT	CAC	TTT	GAT	540
G	P	L	G	V	L	G	H	A	F	P	P	G	L	G	L	G	G	D	T	193
GGT	CCT	CTG	GGA	GTC	CTT	GGC	CAT	GCC	TTT	CCT	CCT	GGT	CTG	GGT	CTA	GGT	GGT	GAC	ACT	600
H	F	D	E	D	E	T	W	I	A	K	D	G	E	G	F	N	L	F	L	213
CAC	TTT	GAC	GAA	GAT	GAA	ACA	TGG	ATA	GCC	AAG	GAT	GGG	GAA	GGG	TTC	AAC	TTG	TTT	CTT	660
V	A	A	H	E	F	G	H	S	L	G	L	S	H	S	N	D	Q	T	A	233
GTG	GCT	GCT	CAT	GAA	TTT	GGT	CAC	TCT	CTG	GGG	CTG	TCC	CAC	TCC	AAT	GAT	CAA	ACA	GCC	720
L	M	F	P	N	Y	I	S	L	D	P	S	K	Y	P	L	S	Q	D	D	253
TTG	ATG	TTC	CCC	AAT	TAC	ATC	TCC	CTG	GAT	CCT	AGC	AAA	TAC	CCA	CTT	TCT	CAG	GAT	GAT	780
I	D	G	I	Q	S	I	Y	G	S	P	P	K	V	T	T	K	P	S	G	273
ATT	GAT	GGG	ATC	CAG	TCC	ATC	TAT	GGA	AGT	CCA	CCT	AAG	GTA	ACC	ACC	AAG	CCA	AGT	GGA	840
N	S	E	P	H	A	C	D	P	T	L	T	F	D	A	I	T	T	F	R	293
AAT	TCT	GAA	CCC	CAC	GCC	TGT	GAC	CCC	ACC	TTG	ACT	TTT	GAT	GCT	ATC	ACT	ACT	TTC	CGC	900
R	E	V	M	F	F	K	G	R												302
AGG	GAA	GTT	ATG	TTC	TTT	AAA	GGC	AGG												927

Fig. 15G

TAAACCTATTCCCTTGACACTCCAGCTTCTTATATAAGATGTTTTTTTTTTTCAAGGATCTCCGGATAAACAGTCTTCTA	1007
CTCAGCTAGAAAGCCAGTTGCTGAGCATGTACCAGTACATCAGCAAGAGATTCTTCTCAAGAAACAATGTAGAAACAA	1087
TCAAAGAAAACACCCCAAGGCAACCTGCAGCCTCCACACATAAGCACACATGCATTCACATGTATGCCCCACATATGTGA	1167
ACATGTAGGCACACATGCATGCCATACCACAAACCACAACTTAAGACTGAAACATGCTGATGGACACAGGTACCAGGACA	1247
TCATTGATGAAATATTTTGTGTTTAATGCAGG	1279
H L W R V Y S D I A G A E F E F I D S F	322
CAC TTA TGG AGG GTC TAC TCT GAT ATT GCT GGT GCT GAG TTT GAG TTT ATT GAT TCC TTC	1339
W P S L P A D L Q A A Y E S P R D E L L	342
TGG CCA TCT CTG CCA GCT GAT CTT CAA GCT GCC TAT GAA AGC CCC AGA GAT GAG CTC CTT	1399
V F K D E N F W V I R G Y S V L P G Y P	362
GTT TTT AAA GAT GAG AAT TTC TGG GTC ATC AGG GGA TAT TCT GTC TTC CCC GGT TAC CCC	1459
K S I H T L G F P R R V K K I D A A V C	382
AAA TCC ATC CAC ACA CTC GGA TTT CCA AGA CGT GTG AAG AAA ATT GAT GCA GCC GTC TGT	1519
D H D T R K T F F F V G I W C W R Y D E	402
GAT CAT GAT ACA AGA AAA ACC TTC TTT TTT GGT GGC ATC TGG TGC TGC AGG TAT GAT GAG	1579
M A Q A M D R G F P Q R I I K C F P G I	422
ATG GCA CAA GCA ATG GAC AGA GGA TTC CCA CAG AGG ATA ATA AAG TGC TTC CCA GGA ATT	1639

**Fig. 15H**

R	L	R	V	D	A	V	F	Q	H	N	G	F	L	Y	F	F	H	G	S	442
CGC	CTC	CGT	GTG	GAT	GCT	GTC	TTC	CAA	CAT	AAT	GGA	TTC	CTC	TAT	TTC	TTC	CAT	GGG	TCG	1699
R	Q	F	E	Y	D	M	K	A	K	N	I	T	Q	V	I	K	T	N	S	462
AGG	CAA	TTT	GAA	TAT	GAC	ATG	AAG	GCG	AAA	AAT	ATC	ACC	CAA	GTG	ATC	AAA	ACC	AAT	TCT	1759
W	F	L	C	N	E	P	L	N	A	S	F	N	V	S	V	K	G	K	A	482
TGG	TTC	CTG	TGT	AAC	GAA	CCA	TTA	AAC	GCA	TCA	TTC	AAT	GTC	AGT	GTC	AAA	GGA	AAA	GCA	1819
N	S	I	G	T	V	I	L	H	H	K	R	L	S	L	L	T	F	S	I	502
AAT	TCA	ATT	GGC	ACA	GTG	ATA	TTA	CAT	CAT	AAA	AGG	TTA	AGC	TTG	CTC	ACT	TTC	AGT	ATT	1879
V	H	V	L	T	K	T	Y	N	*											511
GTT	CAT	GTG	CTG	ACA	AAA	ACA	TAC	AAT	TAA	CAATAAA	TTCCACA	AAATAAA	CCAAAA	CAAAATCTTT	TAACC					1949
TGA	ACT	CTG	CC	TCAG	AAG	ACTCA	AGAG	TGG	AGAG	ATG	ACCC	AGTGG	TTAAG	TGC	ACTGG	CTGCTCTT	TCAA	AGG	ACCC	2029
AGG	TTT	GAT	TCT	CAG	TAC	CCAC	ATGG	CAGTCC	CACAG	CTCTCT	GTAACT	CCAG	ACCAG	GGAATCT	GATGCC	CTCTCT	GG			2109
CCT	CTG	AGG	CAC	TGC	ACA	AGC	ATGG	TGC	ATAG	ACATAT	ACATG	CAAG	CAAC	GGCTAT	ATATTAA	AAATAAA	ATG	AAAA		2189
AGT	AAA	ATA	ATT	GAG	CCCA	ATTCT	TTAG	CATCA	AGTTCT	TACTCT	ACTATAT	ATCAG	CTGG	GTAAC	CAATAA	CCAG	TTA			2269
AAG	TAT	CTG	ATTCT	TAA	CAG	TGAAG	TTTAA	ATATG	ACAAAA	ATCTCT	CAC	TTATTT	TGAG	TC	TAA	TATG	ATTG	AT		2349
AAA	CTT	GG	AAAA	ATTAA	AGC	ATG	CTTAA	AAAA	TAAAC	ATTAA	AGCA	ATTCT	TAA	TCCAAAA	AAAA	AAAA	AAAA	AAAA		2429
AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA		2467

**Fig. 15I**



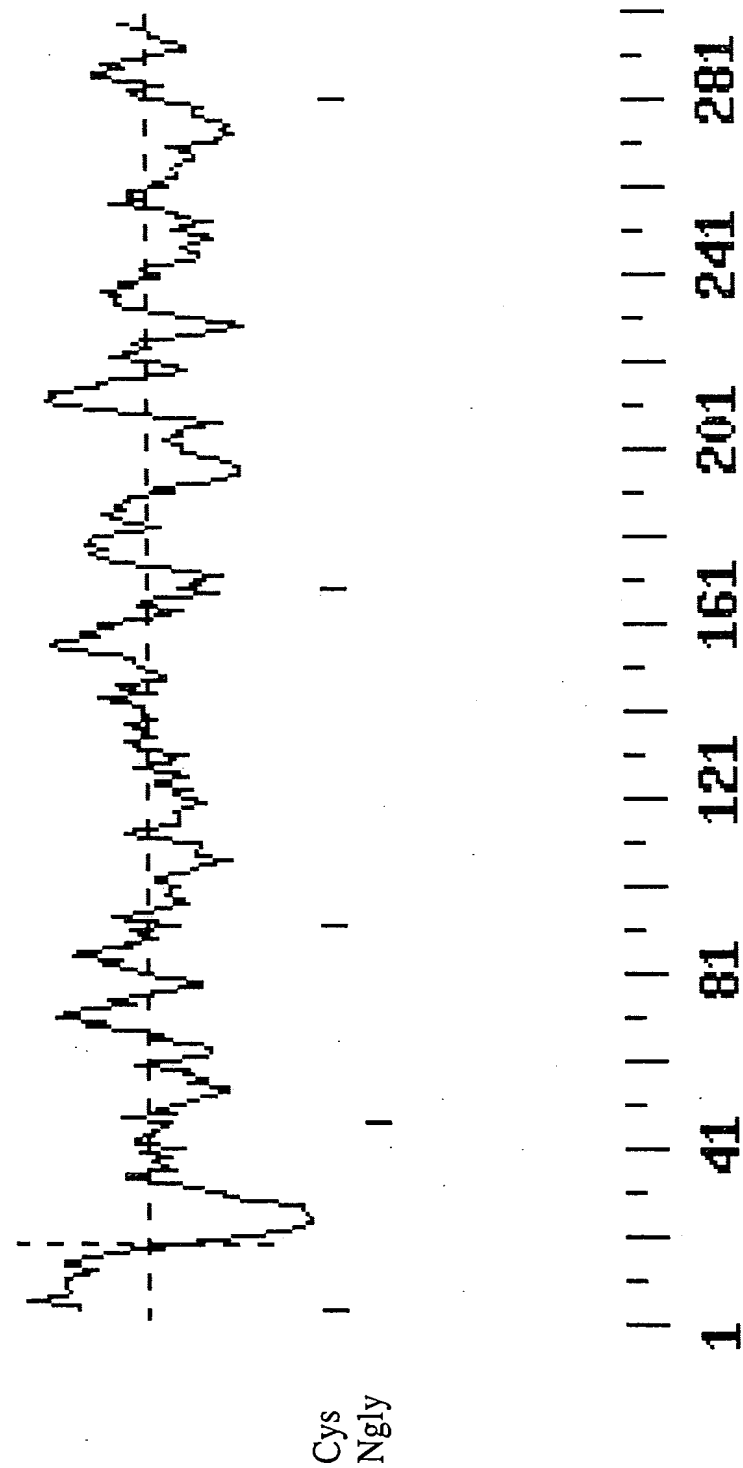


Fig. 15J

human	10	20	30	40	50	60
	MKRLLLFLFFITFSSAFPLVRMTENEENMQAQAYLNQFYSLIEGNHLVQSKNRS	10	20	30	40	50
murine	10	20	30	40	50	60
	SLMVNFITLSAAFPDRKDKNEENNQLAQAYLNQFYSLIEGSHFVQSKNRS	10	20	30	40	50
	FDGKL					
human	70	80	90	100	110	120
	REMQAFFGLTVTGKLDSENTLEIMKTPRCGVPDVQGYGYTLPGWRKY	70	80	90	100	110
murine	70	80	90	100	110	120
	NTLIEIMKTPRCGVPDVQGYGYTLPGWRKYSLTYRIMNYTPDMTPADVDEAIQK	70	80	90	100	110
	130					
human	140	150	160	170	180	190
	GLEVWSKVTPCLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGVLGHAFPPG	140	150	160	170	180
murine	140	150	160	170	180	190
	PLGGLGGDTHFDEDETNW-T	140	150	160	170	180
	ALQVWSKVTPLTFTTRISKGVADIMIAFRTGVGHCPRHFDGPLGVLGHAFPPG	140	150	160	170	180
	GLGGLGGDTHFDEDETWIA	140	150	160	170	180
	200					
human	210	220	230	240	250	260
	KDGAGFNFLVAAHEFGHALGLSHSNDQTALMFPNYVSLDPRKYPLSQDDINGIQ	210	220	230	240	250
murine	210	220	230	240	250	260
	SIYGGLPKVPKPKPE	210	220	230	240	250
	KDGEGFNFLVAAHEFGHSLGLSHSNDQTALMFPNYISLDPSKYPLSQDDIDG	210	220	230	240	250
	SIYGSPPKVTTKPSG	210	220	230	240	250
	270					

**Fig. 15K**

	280	290	300	310	320	330	340
human	PTIPHACDPDLTFDAIT	TFRRREVMFFKGRHLWRIYYDITDVEFFELIASFWPSLPADLQAAAYENPRDKILV					
	.	.....	.....	.....	.....	.....	.....
murine	NSEPHACDPDLTFDAIT	TFRRREVMFFKGRHLWRVYS	DIAGAEFFIDSF	WPSLPADLQAAAYESPRDELLV			
	280	290	300	310	320	330	340
human	FKDENFWMIRGYAVLPDY	PKSIHTLGFPGRVKKIDAAVCDKTT	TRKTYFFVGIWCWRFDEMTQTMDKGFPQ				
	.....	.....	.....	.....	.....	.....	.....
murine	FKDENFWVIRGYSVLP	GYPKSIHTLGFPRRVKKIDAAVCDHD	TRKTTFFVGIWCWRYDEMAQAAMDRGFPQ				
	350	360	370	380	390	400	410
human	RVVKHFPGISIRVDAA	FQYKGFFFSRGSQ	QFEYNIKT	KNITRIMRTNTWFQCKE	PKNSSFGFDINKEKA		
	.....	.....	.....	.....	.....	.....	.....
murine	RIIKCFPGIRLRVDA	VFQHN	GFLYFFHGS	RQFEYDMKAKNITQVIKTNSWFLCNEPLNASFN	SV-KGKA		
	420	430	440	450	460	470	480
human	HSGGIKILYHKSLSL	FIFGIVHLLKNTSIYQ					
	.....	.....	.....	.....	.....	.....	.....
murine	NSIGTVILHHKRLSL	LLTFSIVHVLTKTYN					
	490	500	510				

Fig. 15L

[illegible]

**Fig. 15M**

human	290	300	310	320	330	340	350
	CTCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGGTGCCCTGATGTGGGCCAGTATGGCTACACC						
murine	260	270	280	290	300	310	320
	TTCAGACACACTTTGCGATCATGAAAGTGCCCAAGTGTGGGTACCCAGATGTGGGGCAATATGGCTACACA						
human	360	370	380	390	400	410	420
	CTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAAATAATAAATACTACTCCGGATATGGCAGAGCTG						
murine	330	340	350	360	370	380	390
	CTCCCTGGGTGGAGAAAATACAGCCTTACATACAGAAATAATGAACCTATACTCCTGATATGACACCCAGCTG						
human	430	440	450	460	470	480	490
	CTGTGGATGAGGCTATCCAAAGAAGTTTAGAAGTGTGGAGCAAAAGTCACCTCCACTAAAAATTCACCAAGAT						
murine	400	410	420	430	440	450	460
	ATGTGGATGAGGCTATTTCAGAAAGCTCTACAAGTTTGGAGCAAGGTCACCTCCACTGACGTTTACCCAGGAT						
human	500	510	520	530	540	550	560
	TTCAAAGGGGATTGCAGACATCATGATTGCCCTTTAGGACTCGAGTCCCATGGTCCGGTGTCCCTCGCTATTTT						
murine	470	480	490	500	510	520	530
	ATCCAAGGGGTTGCAGATATAATGATAGCATTCAGGACAGGAGTCCCATGGTGGTGTCCCTCGTCACTTT						

**Fig. 15N**

human	570	580	590	600	610	620	630
	GATGGTCCCTTGGGAGTGCTTGGCCATGCCTTTCCTCCTGGTCCGGGCTCTGGGTGGTGACACTCATTTTG						
murine	540	550	560	570	580	590	600
	GATGGTCCCTCTGGGAGTCCTTGGCCATGCCTTTCCTCCTGGTCTGGGTCTAGGTGGTGACACTCACTTTTG						
human	640	650	660	670	680	690	
	ATGAGGATGAAAACTGGA--CCAAGGATGGAGCAGGATTCAACTTGTTCCTTGTGGCTGCTCATGAATT						
murine	610	620	630	640	650	660	670
	ACGAAGATGAACAATGGATAGCCAAGGATGGGAAGGTTCAACTTGTTCCTTGTGGCTGCTCATGAATT						
human	700	710	720	730	740	750	760
	TGGTCATGCACTGGGGCTCTCTCACTCCAATGATCAAAACAGCCCTTGATGTTCCCAAATTATGTCTCCCTG						
murine	680	690	700	710	720	730	740
	TGGTCACTCTCTGGGGCTGTCCCACCTCCAATGATCAAAACAGCCCTTGATGTTCCCAAATTACATCTCCCTG						
human	770	780	790	800	810	820	830
	GATCCCAGAAAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCCATCTATGGAGGTCTGCCTA						
murine	750	760	770	780	790	800	810
	GATCCTAGCAAAATACCCACTTTCTCAGGATGATATTGATGGGATCCAGTCCCATCTATGGAAGTCCACCTA						

Fig. 150

```

      840      850      860      870      880      890      900
human  AGGTACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCTGTGACCCCTGACTTTGACGCTAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine AGGTAACCAACCAAGCCAAGTGGAATTCCTGAACCCCAAGCCCTGTGACCCCACTTGACTTTTGATGCTAT
      820      830      840      850      860      870      880

      910      920      930      940
human  CACAACCTTCCGCAGAGAGTAATGTTCTTTAAAGGCAGG-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine CACTACTTTCGCAGGGAAGTTATGTTCTTTAAAGGCAGGTAAACCTATTCCCCTTGACACTCCAGCTTCT
      890      900      910      920      930      940      950

human  -----

murine TATAAGATGTTTTTTTTTTTCAAGGATCTCCGGATAAACAGTCTTCTACTCAGCTAGAAAGCCAGTTG
      960      970      980      990      1000      1010      1020

human  -----

murine CTGAGCATGTACCAGTACATCAGCAAGAGATTCTTCCTCAAGAAACAATGTAGAAACAATCAAAGAAAA
      1030      1040      1050      1060      1070      1080      1090

```

**Fig. 15P**

[illegible]

**Fig. 15Q**



	1050	1060	1070	1080	1090	1100	1110
human	GAACCC	CAGAGATAAGATTCTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGGATATGCTGCTTGG					
	1380	1390	1400	1410	1420	1430	1440
murine	AAGCCCC	CAGAGATGAGCTCCTTGTTTTTAAAGATGAGAAATTTCTGGGTCAATCAGGGGATATTCTGTCTTGG					
	1120	1130	1140	1150	1160	1170	1180
human	CCAGATTATCCCAAATCCATCCATACATTAGGTTTTCCAGGACGTGTGAAGAAATAGATGCAGCCGTCT						
	1450	1460	1470	1480	1490	1500	1510
murine	CCCGGTTACCCCAAATCCATCCACACACTCGGATTTCCAAAGACGTGTGAAGAAATTTGATGCAGCCGTCT						
	1190	1200	1210	1220	1230	1240	1250
human	GTGATAAGACCACAAAGAAAAACCTACTTCTTTGTGGGCATTTGGTGCTGGAGGTTTGATGAAATGACCCA						
	1520	1530	1540	1550	1560	1570	1580
murine	GTGATCATGATACAAAGAAAAACCTTCTTTTGTGGCATCTGGTCTGGAGGTATGATGAGATGGCACA						
	1260	1270	1280	1290	1300	1310	1320
human	AACCATGGACAAAGGATTCCCGCAGAGAGTGGTAAACACTTTCTCTGGAATCAGTATCCCGTTGATGCT						
	1590	1600	1610	1620	1630	1640	1650
murine	AGCAATGGACAGAGGATTCCACAGAGGATAATAAAGTGCTTCCCAGGAATTCGCCTCCCGTGTGGATGCT						

**Fig. 15R**

	1330	1340	1350	1360	1370	1380	1390
human	GCTTTCAGTACAAAGGATTCTTTTCAGCCGGATCAAAGCAATTGAATACAACATTAAAGACAA						
	:	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :
murine	GTC TTCCAACATAAATGGATT CCTCTATTTCTTCCATGGGT CAGGCCAATTTGAATATGACATGAAGCGGA						
	1660	1670	1680	1690	1700	1710	1720
human	1400	1410	1420	1430	1440	1450	1460
	AGAA TATTACC CGAATCATGAGAACTAATACTTG GTTCAATGCAAAGAACCAAGACTCCTCATTTGG						
	:	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :
murine	AAAATATCACCCCAAGTGATCAAAACCAATTCTTGGTTCCTGTGTACGAAACCATTAACGCATCATTCAA						
	1730	1740	1750	1760	1770	1780	1790
human	1470	1480	1490	1500	1510	1520	1530
	TTTTGATATCAACAAGGAAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATAGAAGTTTAAGCTTG						
	:	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :
murine	TGTCAGTGTCA--AAGGAAAAGCAAAATTCAATTGGCACAGTGATATTACATCATATAAAGTTAAGCTTG						
	1800	1810	1820	1830	1840	1850	1860
human	1540	1550	1560	1570	1580	1590	1600
	TTTATTTTGGTATTGTTTCATTTGCTGAAAAACACTTCTATTTATCAATAAATTC-----ATAGACCTAA						
	:	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :
murine	CTC ACTTTCAGTATTGTTTCATGTGCTGACAAAAACATACAAATTAAACAATAAATCCACAATAAACC AAA						
	1870	1880	1890	1900	1910	1920	1930

**Fig. 15S**

human	A-----ATAAACCT-----CAACAGG-----	1610
:	: .:::.:::	
murine	ACAAATCTTTTAACCTGAACCTCTGCCTCAGGAAGACTCAAGAGTGGAGAGATGACCCAGTGTTAAGTG	1940    1950    1960    1970    1980    1990    2000
human	-----TCCTTTTAATA-----TAAATTCT-----	1620                  1630
:	: .:::.:::	
murine	CAC TGG CTGC TCT TTCAA AGG ACC CAG GTT TG AT TCT CAG TACC CACA TGG CAG TC CAC AG CTCT CTGT GA	2010    2020    2030    2040    2050    2060    2070
human	-----GCTTC-----	
:	: : :	
murine	ACTCCAGACCCAGGAAATCTGATGCCCTCTCTGGCCCTCTGAGGGCACTGCACAAGCATGTGTCATAGAC	2080    2090    2100    2110    2120    2130    2140
human	-----AAAATAGAATAAAA-----	1640                  1650
:	: .:::.:::	
murine	ATATACATGCAAGCAAACGGCTATATATTTAAATAAAATGAAAAAGTAAATAATTGAGCCCCAATTCTT	2150    2160    2170    2180    2190    2200    2210

**Fig. 15T**

human	1670	TAACAACAA-----	
		::::::	
murine		TAGCATCAAGTTCTTACTCCTACTATATATCAGCTGGGTAACCAATAACCAAGTTAAAGTATCTGATTC	2280
	2220	2230 2240 2250 2260 2270	
human		-----	
murine		CTAACAGTGAAGTTTAAATATGACAAAAATCTCTCACTTATTTTGAGTCTAAATTAATGATTTGC	2350
	2290	2300 2310 2320 2330 2340	
human		-----	
murine		TGGAAAAATTAAAGCATGTCCTTAAAAATAAACATTAAAGACAATTCTTAATCCAAAA	2420
	2360	2370 2380 2390 2400 2410	
human		-----	
	1680	-----AAAA	
		::::::	
murine		AAAAAAAAAAAAAAAAAAAAAAAA	2460
	2430	2440 2450	

**Fig. 15U**

	10	20	30	40	50	60
210 M---	KRLLLFLFFITFSSAFPLVRMTENEENMQLAQAYLNQFYSLIEGHNHLVQSKNRSLIDDKIREMQ					
MMP-8	MFSLKTLPFLLLLHVQISKAFPV---SSKEKNTKTVQDYLEKFYQLPSNQYQSTRKNGTNVIVEKLKEMQ					
	70	80	90	100	110	120
210 AFFGLT	VTGKLDSENTLEIMKTPRCGVPDVGYTYTL--PGWRKYNLTYRIINYPDMARAAVDEAIQEGL					
MMP-8	RFFGLNVTGKPNEETLDMMKKPRCGVPDSGGFMLTPGNPKWERTNLTYRIRNYTPQLSEAEVERAIKDAF					
	140	150	160	170	180	190
210 EVWSKV	TPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGVLGHAFFPPGPGGGDTHFDEDENWTKDGD					
MMP-8	ELWSVASPLIFTRISQGEADINIAFYQRDHGDNRP-FDGPNGILAHAFQPQGIGGDAHFAEETWNTS					
	210	220	230	240	250	260
210 AGFNLF	VAAHEFGHALGLSHSNDQTALMFNPVVS�DPKYPPLSQDDINGIQSIYGGLPKVPKPKPEPTI					
MMP-8	ANYNFLVA AH EFGHSLGLAHSSDPGALMYPNYAFRETSNYSLPQDDIDIGIQAIYG-LSSNPIQPTGPST					

**Fig. 15V**

[illegible]

**Fig. 15W**

```

10      20      30      40      50      60
210 ATGAAGCGCCCTTCT---GCTTCTGTGTTTTGTTCTTTATATAACATTTTCT-TCTGCAATTTCCCTTAGTCCG
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 ATGTT-CTCCCTGAAGACGCTTCCATTTCTGCTCTTACTC-CATGTGCAGATTTCCAAGGCCCTT--TCCT
    10      20      30      40      50      60

70      80      90      100     110     120     130
210 GATGACGGAAATGAAGAAATA-TGCAACTGGCTCAGGCATATCTCAACCAGTTCTACTCTCTTGAAAT
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 G-TATCTTCTAAAGAGAAATAACAAAACTGT-TCAGGACTACCTGGAAAAAGTTCTAC-CAATTACCAA
    70      80      90      100     110     120     130

140     150     160     170     180     190     200
210 AGAAG-GGAATCATCTTGTTCAAAGCAAGAATAG---GAGTCTCATAGATGACAAAATTCGGGAAATGCA
    . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 GCAACCAGTATCAG--TCTACAAGG-AAGAATGGCACTAATGTGATCGTTGAAAAGCTTAAAGAAATGCA
    140     150     160     170     180     190     200

210     220     230     240     250     260     270
210 AGCATTTTTTGGATTGACAGTGACTGGAAAACTGGACTCAAACACCCCTTGAGATCATGAAGACACCCAGG
    . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 GCGATTTTTTGGGTTGAATGTGACGGGGAAGCCAAATGAGGAAACTCTGGACATGATGAAAAAGCCTCGC
    210     220     230     240     250     260     270

```

**Fig. 15X-1**

	280	290	300	310	320	330
210	TGTGGGTCCTGA-TGTGG-GCCAGTATGGCTACACC-----TCCCTGGTGAGAAAAATAACAACCTCA					
MMP-8	: :					
	280	290	300	310	320	330
	TGTGGAGTGCCTGACAGTGGTGGTTTATATTAAACCCAGGAAACCCCAAAGTGGGAACGCCACTAACTTGA					
	:	:	:	:	:	:
	340	350	360	370	380	390
210	CCTACAGAATAATAAACTATACTCCGGGATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAAGAAGGTTT					
MMP-8	: :					
	350	360	370	380	390	400
	CCTACAGGATTTCGAAAACATATACCCCACACAGCTGTCAGAGGCTGAGGTAGAAAGAGCTATCAAGGATGCCCTT					
	:	:	:	:	:	:
	410	420	430	440	450	460
210	AGAAGTGTGGAGCAAAGTCACCTCCACTAAATAATCACCAAAGATTTCAAAGGGGATTGCAGACATCATGATT					
MMP-8	: :					
	420	430	440	450	460	470
	TGAACCTCTGGAGTGTTCATCACCTCTCATCTTCACCAGGATCTCACAGGAGAGGCAGATATCAACATT					
	:	:	:	:	:	:
	480	490	500	510	520	530
210	GCCTTTAGGACTCGAGTCCATGGTCGGTGTCTCCCTCGCTATTTTGATGGTCCCTTGGGAGTGCTTGGCCATG					
MMP-8	: : : : : . :					
	490	500	510	520	530	540
	GCTTTTTTACCAAAAGAGATCACGGTGACAATCTCTC-C-A--TTTGATGAGACCCAATGGAATCCTTGCTCATG					

**Fig. 15X-2**



550	560	570	580	590	600	610	
210	CCTTTCCCTCGTCCGGGTCTGGGTGGTGACACTCATTTTGATGAGGATGAAAACTGGACCAAGGATGG						
	::::: ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: :						
MMP-8	CCTTTCAGCCAGGCCAAGGTATTGGAGGAGATGCTCATTTTGATGCCGAGAAACATGGACCAACACCTC						
550	560	570	580	590	600	610	
620	630	640	650	660	670	680	
210	AGCAGGATTCAACTTGTTTCTTTGTGGCTGCTCATGAATTTGGTCATGCACCTGGGGCTCTCTCACTCCAAT						
	::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: :						
MMP-8	CGCAAAATTACAACCTTGTTTCTTTGTGCTGCTCATGAATTTGGCCATTCTTTGGGGCTCGCTCACTCCTCT						
620	630	640	650	660	670	680	
690	700	710	720	730	740	750	
210	GATCAACAGCCTTGATGTTCCCAAATTAATGTCTCCCTGGATCCCAGAAAAATACCCACTTTCAGGATG						
	:: : .. ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: :						
MMP-8	GACCCCTGGTGCCCTTGATGATATCCCAACTATGCTTTTCAGGAAACCAAGCAACTACTCACTCCCTCAAGATG						
690	700	710	720	730	740	750	
760	770	780	790	800	810	820	
210	ATATCAATGGAATCCAGTCCATCTATGGAGGTCCTGCCCTAAGGTACCTGCTAAGCCAAAGGAACCCACTAT						
	: ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: : ::::: :						
MMP-8	ACATCGATGGCATTCAGGCCATCTATGGA---CTTTCAGCAACCCCTATCCAACTACTGGACCAAGCAC						
760	770	780	790	800	810	820	

**Fig. 15X-3**

```

830      840      850      860      870      880      890
210 ACCCCATGCCCTGTGACCCCTGACTTTGACGCTATCACAACCTTCCGCGAGAGAAATGTTCTTT
MMP-8 ACCCAAACCCCTGTGACCCCGAGTTTGACATTTGATGCTATCACCACACTCCGTGGAGAAATACTTTTCTTT
830      840      850      860      870      880      890

900      910      920      930      940      950      960
210 AAAGGCAGGCACCTATGGAGGAT-CTATTATGATATCACGGATGTTGAGTTTGAATTAATTGCTTCATTC
MMP-8 AAAGACAGGTACTTCTGGAGAAAGGCATCCTCAGCTACAAAGA-GTCGAAATGAATTTTATTCTCTCTATTTC
900      910      920      930      940      950      960

970      980      990      1000      1010      1020      1030
210 TGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCC---CAGAGATAAGATTCTGTGTTTAA
MMP-8 TGGCCATCCCCTTCCAACCTGGTATACAGGCTGCTTATGAAGATTTTGACAGAGACCTCATTTTCCCTATTTA
970      980      990      1000      1010      1020      1030

1040      1050      1060      1070      1080      1090
210 AAGATGAAAACCTTCTGGATGATCAGAGGATATGCTGTCTTGCCAGATTATCCCAAATCCATC-CATACAT
MMP-8 AAGGCAACCAATACTGGGCTCTGAGTGGCTATGATATTCTGCAAGGTTATCCCAAGGATATATCAAAAC-T
1040      1050      1060      1070      1080      1090      1100

```

**Fig. 15X-4**

```

1100      1110      1120      1130      1140      1150      1160
210 TAGGTTTTCAGGACGTGTGAAGAAAAATAGATGCAGCCGCTCTGTGATAAGACCACAAGAAAAACCTACTT
    ::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 ATGGCTTCCCCAGCAGCGTCCAAGCAATTGACGCAGC-----TGTTTCTACAGAAGTAAAAACATACTT
1110      1120      1130      1140      1150      1160

1170      1180      1190      1200      1210      1220      1230
210 CTTTGTGGGCATTTGGTGTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCCGCAGAGA
    ::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 CTTTGTAAATGACCCAATTCTGGAGATATGAT-----AACCAAAGACAATT-----CATGGAGC
1170      1180      1190      1200      1210

1240      1250      1260      1270      1280      1290      1300
210 GTGGTAAACACTTTCCCTGGAATCAGTATCCGTTGTGATGCTGCTTTCAGTACAAAGGATTCTTCTTTT
    ::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 CAGGT-----TATCCCAAAGCA-TATC-----AGGTGC--CTTTCAGGAATAGAGAGTAAA-----
1220      1230      1240      1250      1260

1310      1320      1330      1340      1350      1360      1370
210 TCAGCCGTGGATCAAAGCAATTGAAATACAACATTAAGACAAAGAATATTACCCGAATCATGAGAATAA
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 -----GTTGAT----GCAGTTT---TCCAGCA-----AGAACATTTC-----TTC-----
1270      1280      1290      1300

```

**Fig. 15X-5**

```

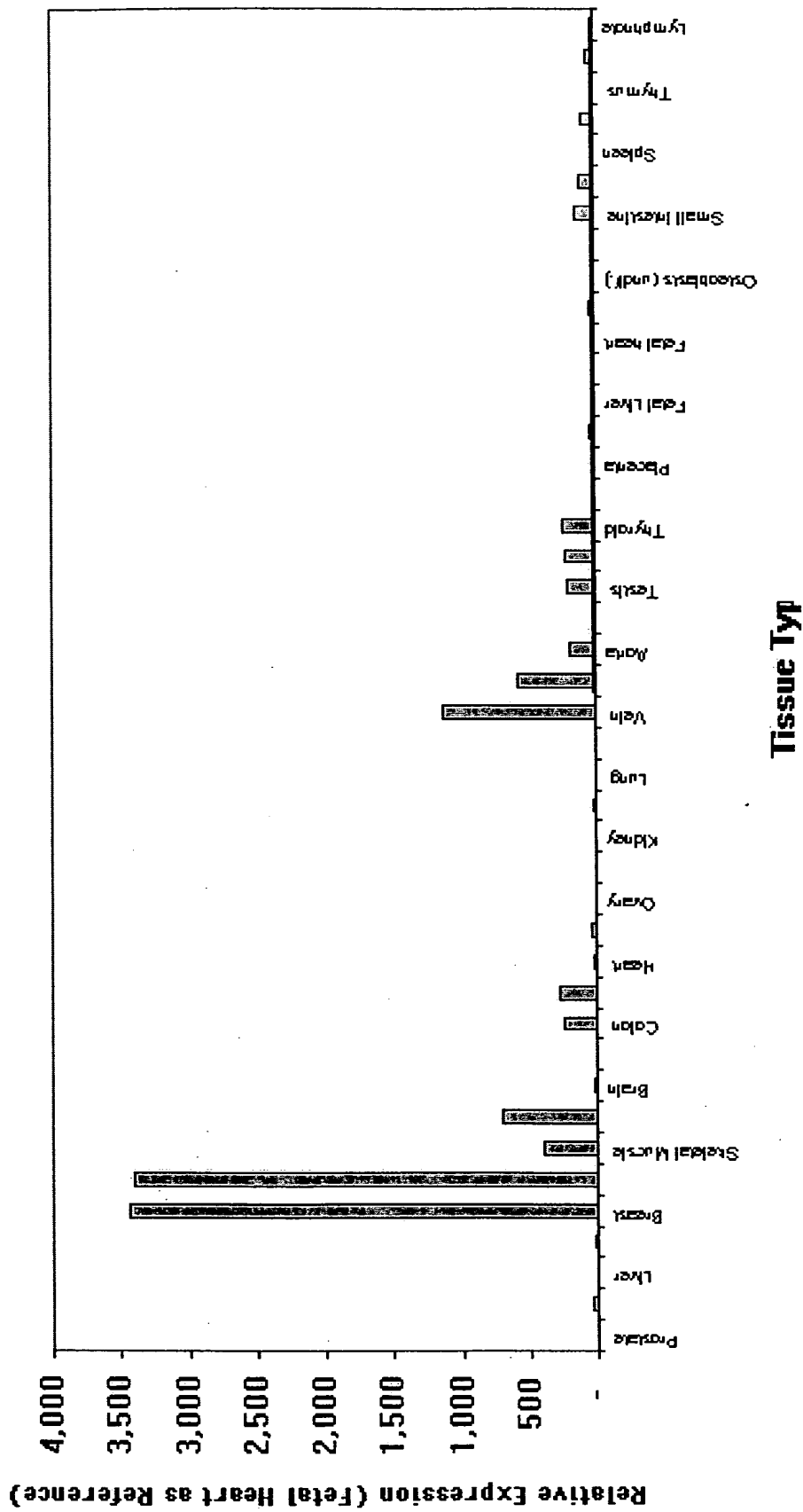
1380      1390      1400      1410      1420      1430      1440
210 TACTTGGTTTCAATGCAAGAACCAGAACTCCTCATTTTGGTTTGTGATATCAACAAGGAAAAAGCACAT
      :.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 --CATG---TC---TTCAGTGGACCAAGATATTACGCATTTGATCTT-ATTGCT-CAGAGAGTTA-C-----
1310      1320      1330      1340      1350

1450      1460      1470      1480      1490      1500      1510
210 TCAGGAGGCATAAAGATATTGTATCATAAAGAGTTTAAGCTTGTTTATTTTGGTATTGTTTCATTGCTGA
      :.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 -CAGA-----GTTGCAAGAG-----GCA-----ATAAATGG-----C-TTAACTGT
1360      1370      1380      1390

1520      1530
210 AAAACACTTCTATTATCAA
      :.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MMP-8 AGA-----TATGGC---
      1400

```

**Fig. 15X-6**



**Fig. 15Y**



S	H	N	Q	L	R	E	V	S	V	S	A	F	T	T	H	S	Q	G	R	158
AGC	CAC	AAC	CAG	CTC	CGG	GAG	GTC	TCA	GTG	TCT	GCC	TTC	ACG	ACG	CAC	AGT	CAG	GGC	CGG	559
A	L	H	V	D	L	S	H	N	L	I	H	R	L	V	P	H	P	T	R	178
GCA	CTA	CAC	GTG	GAC	CTC	TCC	CAC	AAC	CTC	ATT	CAC	CGC	CTC	GTG	CCC	CAC	CCC	ACG	AGG	619
A	G	L	P	A	P	T	I	Q	S	L	N	L	A	W	N	R	L	H	A	198
GCC	GGC	CTG	CCT	GCG	CCC	ACC	ATT	CAG	AGC	CTG	AAC	CTG	GCC	TGG	AAC	CGG	CTC	CAT	GCC	679
V	P	N	L	R	D	L	P	L	R	Y	L	S	L	D	G	N	P	L	A	218
GTG	CCC	AAC	CTC	CGA	GAC	TTG	CCC	CTG	CGC	TAC	CTG	AGC	CTG	GAT	GGG	AAC	CCT	CTA	GCT	739
V	I	G	P	G	A	F	A	G	L	G	G	L	T	H	L	S	L	A	S	238
GTC	ATT	GGT	CCG	GGT	GCC	TTC	GCG	GGG	CTG	GGA	GGC	CTT	ACA	CAC	CTG	TCT	CTG	GCC	AGC	799
L	Q	R	L	P	E	L	A	P	S	G	F	R	E	L	P	G	L	Q	V	258
CTG	CAG	AGG	CTC	CCT	GAG	CTG	GCG	CCC	AGT	GGC	TTC	CGT	GAG	CTA	CCG	GGC	CTG	CAG	GTC	859
L	D	L	S	G	N	P	K	L	N	W	A	G	A	E	V	F	S	G	L	278
CTG	GAC	CTG	TCG	GGC	AAC	CCC	AAG	CTT	AAC	TGG	GCA	GGA	GCT	GAG	GTG	TTT	TCA	GGC	CTG	919
S	S	L	Q	E	L	D	L	S	G	T	N	L	V	P	L	P	E	A	L	298
AGC	TCC	CTG	CAG	GAG	CTG	GAC	CTT	TCG	GGC	ACC	AAC	CTG	GTG	CCC	CTG	CCT	GAG	GCG	CTG	979

**Fig. 16B**

L	L	H	L	L	P	A	L	Q	S	V	S	V	G	Q	D	V	R	C	R	R	318							
CTC	CTC	CAC	CTC	CCG	GCA	CTG	CAG	CTG	AGC	GTC	AGC	GTG	GGC	CAG	GAT	GTG	CGG	TGC	CGG	CGC	1039							
L	V	R	E	G	T	Y	P	P	R	R	P	G	S	S	P	K	V	A	L	H	338							
CTG	GTG	CGG	GAG	GGC	ACC	TAC	CCC	CGG	AGG	CCT	GGC	TCC	AGC	CCC	AAG	GTG	GCC	CTG	CAC	1099								
C	V	D	T	R	E	S	A	A	R	G	P	T	I	L	*						354							
TGC	GTA	GAC	ACC	CGG	GAA	TCT	GCT	GCC	AGG	GGC	CCC	ACC	ATC	TTG	TGA						1147							
CAA	ATG	TG	TG	GGC	CCAC	ATA	CAG	ACT	GTG	TG	TG	CTG	GGG	CTG	CCCT	CAG	GTCC	CCG	AGTAA	CTT	ATG	TTCA	ATGTG	1226				
CCA	ACAC	CAG	GGG	GAG	CCCG	AGC	CTAT	GTG	GCA	GGT	CAC	CAC	AGG	AGT	TGT	GGC	CTAG	GAG	AGG	CTT	TG	GAC	CTT	TGG	ACCT	1305		
GGG	AGCC	ACAC	CTAG	GAG	CAAA	GTCT	CAC	CCCT	TTT	GTCT	ACG	TTG	CTT	CCCC	AAAC	CAT	GAG	CAG	AGG	ACT	TC	GAT	GC			1384		
CAA	ACC	AGAC	TCGG	TCC	CTC	CTT	CCCC	CACT	TAT	CCCC	CAAG	TGCC	TTCC	CTCAT	GCCT	GCC	TGG	CCCG	GCCTG							1463		
ACCC	GCA	ATGG	GCAG	AGGT	GGT	GGG	ACCC	CTG	CTG	CAG	GGC	AGAT	TCA	GGT	CCACT	GGCT	GAG	TG	TGCC	CTT	GG					1542		
GCCC	ATGG	CCCC	AGT	CAT	CAG	GGG	CGAG	TTT	CTT	CTA	ACAT	AG	CCCTT	CTT	TGCC	ATG	AGG	CCAT	GAG	CCCC	CG	CTT				1621		
CAT	CC	TTT	CTAT	TCC	CTAG	AAC	CTT	AAT	GGT	AG	GAAT	TG	CA	AA	GAAT	CA	AGT	CCAC	CCCT	CTCAT	GTG	AC	AGAT			1700		
GGG	AA	ACT	GAG	GCCT	TG	AG	AA	AGG	CTA	ATCT	AAG	TCT	CG	GGC	AGT	GG	CAT	GAG	CAC	AGC	CTC	CT				1779		
GCCT	CC	AG	CCG	AC	CAAT	GCA	CTT	TCT	TG	CTC	CTA	ATA	AG	CCCC	AC	CCCT	CCCG	CTGG	CTC	CCCT	TG	CTGC				1858		
CC	TG	CC	TG	TCC	CA	TAG	CAC	AGG	AGT	AGC	AGC	AGC	AGC	CA	AGC	CTCA	AGT	GG	ACT	CTG	GG	CC	CTG			1937		
ACC	AG	CTG	TG	CGG	CA	TGG	CTA	AGT	CA	CTG	CCCC	TT	CG	GAG	CCCT	CTG	GA	AGCT	TAG	GG	CAC	ATT	GGT	TCC	AGC	CTAGC	2016	
CAG	TT	CT	CAC	CC	TGG	TTGG	GT	CCCC	AG	CA	TCC	AG	ACT	GGA	AA	CC	TAC	CCAT	TTT	CCCC	CTG	AG	CA	TCC	CT	TAGATG	2095	
CTG	CCCC	AAG	GAG	TTG	CTG	CAG	TTCT	TG	GAG	CCCT	CA	CTG	GG	CTG	GGAT	CTC	CA	AGG	GGC	CTC	CTG	GAT	T	CAG	T	CCCC	ACT	2174
GGCC	CTG	AG	CAC	GAC	CCCC	TTCT	TAC	CCCT	CC	CAG	GAAT	TG	CCG	TG	AA	AGG	AG	ACA	AGG	TCT	TG	CCCC	GAC	CC	ATG	TCT	ATG	2253

**Fig. 16C**



CTCTACCCAGGCAGCATCTCAGCTTCCGAACCCCTGGGCTGTTTCCCTTAGTCTTCATTTTATATAAAAGTTGTTGCCCTT 2332  
TTTAACGGAGTGTCACTTTCAACCGGCTCCCTACCCCTGCTGCGCGGATGGAGACATGTCAATTTGTAAAGCAGA 2411  
AAAAGGTGCAATTGTTCACCTTTTGTAAATATTGTCCTGGCCCTGTGTTGGGTGTTGGGGAAGCTGGGCATCAGTGGC 2490  
CACATGGGCATCAGGGGCTGGCCCCACAGAGACCCCCACAGGGCAGTGAGCTCTGTCTTCCCCCACCTGCCCTAGCCCCATC 2569  
ATCTATCTAACCGGTCCTTGATTTAATAAACACTATATAAAAGTTAAATAAAAAA 2628

**Fig. 16D**

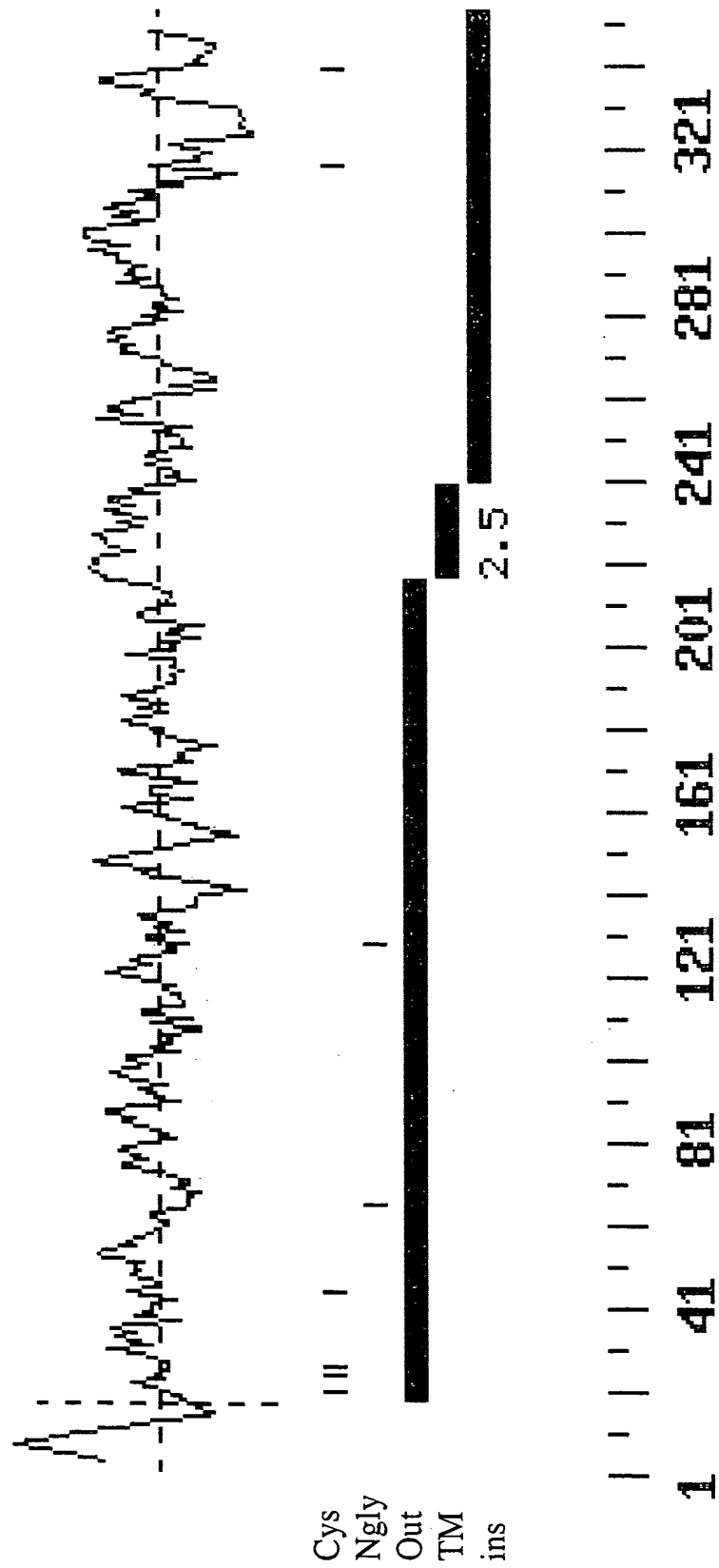


Fig. 16E

GTCGACCCACGCGTCCGCCCGCCCTAGCGCCGCGGGTCCGCCGAGCCGAGCCGAGCGGAGCCGGGAGCCTC	79
TGGAATCACCCGGGTCGCTGTTCTGAGGTGGTCAAGGTGGACAGGGGCGGTGGTGTATGGCGCAGTTTGACACTGAAT	158
ACCAGCGCCTAGAGGCCTCCTATAGTGATTACACCCCGAGGAGGAGACCTGTTGGTGACAGTCGCCGAGGGAGCAA	237
GTCACCTTGGCACCATATTGAAACCTTGACCTCTTCTCTCTCGAGTTTATAATCTGCACACAGAAATGGCTTCACA	316
M L I G E I F E L M Q F L F V V A F T	19
TGT ATG CTC ATC GGG GAG ATC TTT GAG CTC ATG CAG TTC CTC TTT GTG GTT GCC TTC ACT	376
T F L V S C V D Y D I L L F A N K M V N H	39
ACC TTC CTG GTC AGC TGC GTG GAC TAT GAC ATC ATC CTA TTT GCC AAC AAG ATG GTG AAC CAC	436
S L H P T E P V K V T L L P D A F L P A Q	59
AGT CTT CAC CCT ACT GAA CCC GTC AAG GTC ACT CTG CCA GAC GCC TTT TTG CCT GCT CAA	496
V C S A R I Q E N G S L L I T I L V I A G	79
GTC TGT AGT GCC AGG ATT CAG GAA AAT GGC TCC TCT ATC ACC ATC CTG GTC ATT GCT GGT	556
V F W I H R L I K F I Y N I C C Y W E I	99
GTC TTC TGG ATC CAC CGG CTT ATC AAG TTC ATC TAT AAC ATT TGC TGC TAC TGG GAG ATC	616
H S F Y L H A L R I P M S A L P Y C T W	119
CAC TCC TTC TAC CTG CAC GCT CTG CGC ATC CCT ATG TCT GCC CTT CCG TAT TGC ACG TGG	676

**Fig. 17A**

Q	E	V	Q	A	R	I	V	Q	T	Q	K	E	H	Q	I	C	I	H	K	139
CAA	GAA	GTG	CAG	GCC	CGG	ATC	GTG	CAG	ACG	CAG	AAG	GAG	CAC	CAG	ATC	TGC	ATC	CAC	AAA	736
R	E	L	T	E	L	D	I	Y	H	R	I	L	R	F	Q	N	Y	M	V	159
CGT	GAG	CTG	ACA	GAA	CTG	GAC	ATC	TAC	CAC	CAC	ATC	CTC	CGT	TTC	CAG	AAC	TAC	ATG	GTG	796
A	L	V	N	K	S	L	L	P	L	R	F	R	L	P	G	L	G	E	A	179
GCA	CTG	GTT	AAC	AAA	TCC	CTC	CTG	CCT	CTG	CGC	TTC	CGC	CTG	CCT	GGC	CTC	GGG	GAA	GCT	856
V	F	F	T	R	G	L	K	Y	N	F	E	L	I	L	F	W	G	P	G	199
GTC	TTC	TTC	ACC	CGT	GGT	CTC	AAG	TAC	AAC	TTT	GAG	CTG	ATC	CTC	TTC	TGG	GGA	CCT	GGC	916
S	L	F	L	N	E	W	S	L	K	A	E	Y	K	R	G	G	Q	R	L	219
TCT	CTG	TTT	CTC	AAT	GAA	TGG	AGC	CTC	AAG	GCC	GAG	TAC	AAA	CGT	GGG	GGG	CAA	CGG	CTA	976
E	L	A	Q	R	L	S	N	R	I	L	W	I	G	I	A	N	F	L	L	239
GAG	CTG	GCC	CAG	CGC	CTC	AGC	AAC	CGC	ATC	CTG	TGG	ATT	GGC	ATC	GCT	AAC	TTC	CTG	CTG	1036
C	P	L	I	L	I	W	Q	I	L	Y	A	F	F	S	Y	A	E	V	L	259
TGC	CCC	CTC	ATC	CTC	ATA	TGG	CAA	ATC	CTC	TAT	GCC	TTC	TTC	AGC	TAT	GCT	GAG	GTG	CTG	1096
K	R	E	P	G	A	L	G	A	R	C	W	S	L	Y	G	R	C	Y	L	279
AAG	CGG	GAG	CCG	GGG	GCC	CTG	GGA	GCA	CGC	TGC	TGG	TCA	CTC	TAT	GGC	CGC	TGC	TAC	CTC	1156

**Fig. 17B**

R	H	F	N	E	L	E	H	E	L	Q	S	R	L	N	R	G	Y	K	P	299
CGC	CAC	TTC	AAC	GAG	CTG	GAG	CAC	GAG	CTG	CAG	TCC	CGC	CTC	AAC	CGT	GGC	TAC	AAG	CCC	1216
A	S	K	Y	M	N	C	F	L	S	P	L	L	T	L	L	A	K	N	G	319
GCC	TCC	AAG	TAC	ATG	AAT	TGC	TTC	TTG	TCA	CCT	CTT	TTG	ACA	CTG	CTG	GCC	AAG	AAT	GGA	1276
A	F	F	A	G	S	I	L	A	V	L	I	A	L	T	I	Y	D	E	D	339
GCC	TTC	TTC	GCT	GGC	TCC	ATC	CTG	GCT	GTG	CTT	ATT	GCC	CTC	ACC	ATT	TAT	GAC	GAA	GAT	1336
V	L	A	V	E	H	V	L	T	T	V	T	L	L	G	V	T	V	T	V	359
GTG	TTG	GCT	GTG	GAA	CAT	GTG	CTG	ACC	ACC	GTC	ACA	CTC	CTG	CTG	GTC	ACC	GTG	ACC	GTG	1396
C	R	S	F	I	P	D	Q	H	M	V	F	C	P	E	Q	L	L	R	V	379
TGC	AGG	TCC	TTT	ATC	CCG	GAC	CAG	CAC	ATG	GTG	TTC	TGC	CCT	GAG	CAG	CTG	CTC	CGC	GTG	1456
I	L	A	H	I	H	Y	M	P	D	H	W	Q	G	N	A	H	R	S	Q	399
ATC	CTC	GCT	CAC	ATC	CAC	TAC	ATG	CCT	GAC	CAC	TGG	CAG	GGT	AAT	GCC	CAC	CGC	TCG	CAG	1516
T	R	D	E	F	A	Q	L	F	Q	Y	K	A	V	F	I	L	E	E	L	419
ACC	CGG	GAC	GAG	TTT	GCC	CAG	CTC	TTC	CAG	TAC	AAG	GCA	GTG	TTC	ATT	TTG	GAA	GAG	TTG	1576
L	S	P	I	V	T	P	L	I	L	I	F	C	L	R	P	R	A	L	E	439
CTG	AGC	CCC	ATT	GTC	ACA	CCC	CTC	ATC	CTC	ATC	TTC	TGC	CTG	CGC	CCA	CGG	GCC	CTG	GAG	1636

**Fig. 17C**

I	I	D	F	F	TTC	TTC	CGA	AAC	TTC	ACC	GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC	S	459
ATT	ATA	GAC	TTC	TTC	CGA	AAC	TTC	ACC	GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC			1696	
F	A	Q	M	D	GAT	GAT	GTT	CGC	CAG	CAT	GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGG	CAG	ACA	T	479
TTT	GCT	CAG	ATG	ATG	GAT	GAT	GTT	CGC	CAG	CAT	GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGG	CAG	ACA	1756	
E	A	S	V	Y	TAC	TAC	CAG	CAA	GCT	GAG	GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT	F	499
GAG	GCC	TCA	GTG	TAC	TAC	CAG	CAA	GCT	GAG	GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT	1816		
A	I	T	N	P	G	G	W	Q	P	P	P	R	E	S	T	A	F	L	G	F	L	519	
GCC	ATC	ACC	AAC	CCT	GGC	TGG	TGG	CAG	CCA	CCA	CGT	GAG	AGC	ACA	GCC	TTC	CTA	GGC	TTC	CTC	1876		
K	E	Q	V	Q	CAG	CGG	GAT	GGA	GCA	GCT	GCT	AGC	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	P	539	
AAG	GAG	CAG	GTT	CAG	CGG	GAT	GGA	GCA	GCT	GCT	AGC	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	CCT	1936		
E	N	A	L	F	T	ACG	TCT	ATC	CAG	TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	AGC	CTT	1996		
GAA	AAT	GCC	CTC	TTT	ACG	TCT	ATC	CAG	TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	AGC	CTT				
I	A	N	V	V	A	G	S	S	S	C	R	G	P	P	L	P	R	D	L	Q	579		
ATC	GCA	AAT	GTG	GTA	GCT	GGC	TCA	TCC	TCC	TGC	CGG	GGC	CCT	CCA	CTG	CCC	AGA	GAC	CTG	CAG	2056		
G	S	R	H	R	A	E	V	A	S	A	L	R	S	F	S	P	L	Q	P		599		
GGC	TCC	AGG	CAC	AGG	GCT	GAA	GTC	GCC	TCT	GCC	CTG	CGC	TCC	TTC	TCC	CCG	CTG	CAA	CCC		2116		

**Fig. 17D**

G	Q	A	P	T	G	R	A	H	S	T	M	T	G	S	G	V	D	A	R	619
GGG	CAG	GCG	CCC	ACA	GGC	CGG	GCT	CAC	AGC	ACC	ATG	ACA	GGC	TCT	GGG	GTG	GAT	GCC	AGG	2176
T	A	S	S	G	S	S	V	W	E	G	Q	L	Q	S	L	V	L	S	E	639
ACA	GCC	AGC	TCC	GGG	AGC	AGC	GTG	TGG	GAA	GGA	CAG	CTG	CAG	CTG	CTG	GTG	CTG	TCA	GAA	2236
Y	A	S	T	E	M	S	L	H	A	L	Y	M	H	Q	L	H	K	Q	Q	659
TAT	GCA	TCC	ACA	GAG	ATG	AGC	CTG	CAT	GCC	CTC	TAT	ATG	CAC	CAG	CTC	CAC	AAG	CAG	CAG	2296
A	Q	A	E	P	E	R	H	V	W	H	R	R	E	S	D	E	S	G	E	679
GCC	CAG	GCT	GAA	CCT	GAG	CGG	CAT	GTA	TGG	CAC	CGC	CGG	GAG	AGT	GAT	GAG	AGT	GGA	GAA	2356
S	A	P	D	E	G	G	E	G	A	R	A	P	Q	S	I	P	R	S	A	699
AGC	GCC	CCT	GAT	GAA	GGG	GGA	GAG	GGC	GCC	CGG	GCC	CCC	CAG	TCT	ATC	CCT	CGC	TCT	GCT	2416
S	Y	P	C	A	A	P	R	P	G	A	P	E	T	T	A	L	H	G	G	719
AGC	TAT	CCC	TGT	GCA	GCA	CCC	CGG	CCT	GGA	GCT	CCT	GAG	ACC	ACC	GCC	CTG	CAT	GGG	GGC	2476
F	Q	R	R	Y	G	G	I	T	D	P	G	T	V	P	R	V	P	S	H	739
TTC	CAG	AGG	CGC	TAC	GGT	GGC	ATC	ACA	GAT	CCT	GGC	ACA	GTG	CCC	AGG	GTT	CCC	TCT	CAT	2536
F	S	R	L	P	L	G	G	W	A	E	D	G	Q	S	A	S	R	H	P	759
TTC	TCT	CGG	CTG	CCT	CTT	GGA	GGG	TGG	GCA	GAA	GAT	GGG	CAG	TCG	GCA	TCA	AGG	CAC	CCT	2596

**Fig. 17E**





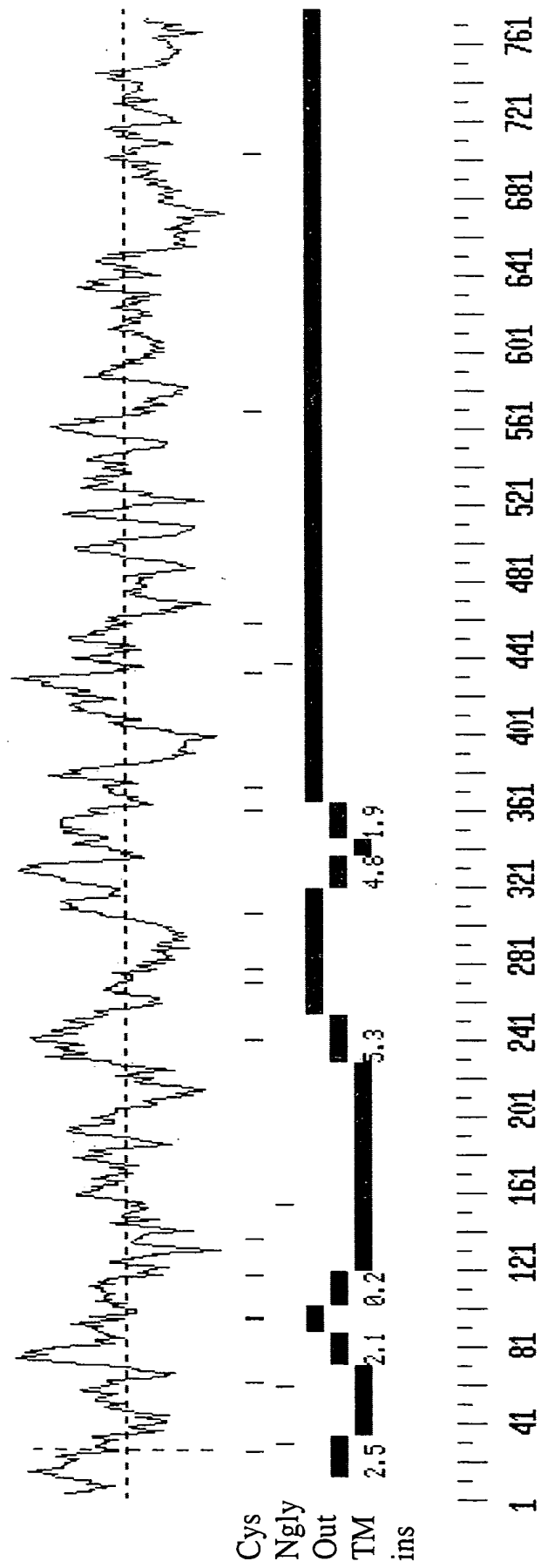


Fig. 17G

CCCCGCCCTAGCGCCGCGGTCTCGCGCCGAGCCGAGCCGAGCCGAGCCGCGGAGCCTCTGGAATCACCCGGGTCG	79
M A Q F D T E Y Q	
CTGTTCTGAGGTGGTCAAGGTGGACAGGGCGGTGGTG ATG GCG CAG TTT GAC ACT GAA TAC CAG	9 146
R L E A S Y S D S P P G E D L L V H V	29
CGC CTA GAG GCC TCC TAT AGT GAT TCA CCC CCA GGG GAG GAG GAC CTG TTG GTG CAC GTC	206
A E G S K S P W H H I E N L D L F F S R	49
GCC GAG GGG AGC AAG TCA CCT TGG CAC CAT ATT GAA AAC CTT GAC CTC TTC TTC TCT CGA	266
V Y N L H Q K N G F T C M L I G E I F E	69
GTT TAT AAT CTG CAC CAG AAG AAT GGC TTC ACA TGT ATG CTC ATC GGG GAG ATC TTT GAG	326
L M Q F L F V V A F T T F L V S C V D Y	89
CTC ATG CAG TTC CTC TTT GTG GTT GCC TTC ACT ACC TTC CTG GTC AGC TGC GTG GAC TAT	386
D I L F A N K M V N H S L H P T E P V K	109
GAC ATC CTA TTT GCC AAC AAG ATG GTG AAC CAC AGT CTT CAC CCT ACT GAA CCC GTC AAG	446
V T L P D A F L P A Q V C S A R I Q E N	129
GTC ACT CTG CCA GAC GCC TTT TTG CCT GCT CAA GTC TGT AGT GCC AGG ATT CAG GAA AAT	506

**Fig. 17H**

G	S	L	I	T	I	L	V	I	A	G	V	F	W	I	H	R	L	I	K	149
GGC	TCC	CTT	ATC	ACC	ATC	CTG	GTC	ATT	GCT	GGT	GTC	TTC	TGG	ATC	CAC	CGG	CTT	ATC	AAG	566
F	I	Y	N	I	C	C	Y	W	E	I	H	S	F	Y	L	H	A	L	R	169
TTC	ATC	TAT	AAC	ATT	TGC	TGC	TAC	TGG	GAG	ATC	CAC	TCC	TTC	TAC	CTG	CAC	GCT	CTG	CGC	626
I	P	M	S	A	L	P	Y	C	T	W	Q	E	V	Q	A	R	I	V	Q	189
ATC	CCT	ATG	TCT	GCC	CTT	CCG	TAT	TGC	ACG	TGG	CAA	GAA	GAT	CAG	GCC	CGG	ATC	GTG	CAG	686
T	Q	K	E	H	Q	I	C	I	H	K	R	E	L	T	E	L	D	I	Y	209
ACG	CAG	AAG	GAG	CAC	CAG	ATC	TGC	ATC	CAC	AAA	CGT	GAG	CTG	ACA	GAA	CTG	GAC	ATC	TAC	746
H	R	I	L	R	F	Q	N	Y	M	V	A	L	V	N	K	S	L	L	P	229
CAC	CGC	ATC	CTC	CGT	TTC	CAG	AAC	TAC	ATG	GTG	GCA	CTG	GTT	AAC	AAA	TCC	CTC	CTG	CCT	806
L	R	F	R	L	P	G	L	G	E	A	V	F	F	T	R	G	L	K	Y	249
CTG	CGC	TTC	CGC	CTG	CCT	GGC	CTC	GGG	GAA	GCT	GTC	TTC	TTC	ACC	CGT	GGT	CTC	AAG	TAC	866
N	F	E	L	I	L	F	W	G	P	G	S	L	F	L	N	E	W	S	L	269
AAC	TTT	GAG	CTG	ATC	CTC	TTC	TGG	GGA	CCT	GGC	TCT	CTG	TTT	CTC	AAT	GAA	TGG	AGC	CTC	926
K	A	E	Y	K	R	G	G	Q	R	L	E	L	L	A	Q	R	L	S	N	289
AAG	GCC	GAG	TAC	AAA	CGT	GGG	GGG	CAA	CGG	CTA	GAG	CTG	GCC	CAG	CGC	CTC	AGC	AAC	CGC	986

**Fig. 17I**

I	L	W	I	G	I	A	N	F	L	L	C	P	L	I	L	I	W	Q	I	309
ATC	CTG	TGG	ATT	GGC	ATC	GCT	AAC	TTC	CTG	CTG	TGC	CCC	CTC	ATC	CTC	ATA	TGG	CAA	ATC	1046
L	Y	A	F	F	S	Y	A	E	V	L	K	R	E	P	G	A	L	G	A	329
CTC	TAT	GCC	TTC	TTC	AGC	TAT	GCT	GAG	GTG	CTG	AAG	CGG	GAG	CCG	GGG	GCC	CTG	GGA	GCA	1106
R	C	W	S	L	Y	G	R	C	Y	L	R	H	F	N	E	L	E	H	E	349
CGC	TGC	TGG	TCA	CTC	TAT	GGC	CGC	TGC	TAC	CTC	CGC	CAC	TTC	AAC	GAG	CTG	GAG	CAC	GAG	1166
L	Q	S	R	L	N	R	G	Y	K	P	A	S	K	Y	M	N	C	F	L	369
CTG	CAG	TCC	CGC	CTC	AAC	CGT	GGC	TAC	AAG	CCC	GCC	TCC	AAG	TAC	ATG	AAT	TGC	TTC	TTG	1226
S	P	L	L	T	L	L	A	K	N	G	A	F	F	A	G	S	I	L	A	389
TCA	CCT	CTT	TTG	ACA	CTG	CTG	GCC	AAG	AAT	GGA	GCC	TTC	TTC	GCT	GGC	TCC	ATC	CTG	GCT	1286
V	L	I	A	L	T	I	Y	D	E	D	V	L	A	V	E	H	V	L	T	409
GTG	CTT	ATT	GCC	CTC	ACC	ATT	TAT	GAC	GAA	GAT	GTG	TTG	GCT	GTG	GAA	CAT	GTG	CTG	ACC	1346
T	V	T	L	L	G	V	T	V	T	V	C	R	S	F	I	P	D	Q	H	429
ACC	GTC	ACA	CTC	CTG	GGG	GTC	ACC	GTG	ACC	GTG	TGC	AGG	TCC	TTT	ATC	CCG	GAC	CAG	CAC	1406
M	V	F	C	P	E	Q	L	L	R	V	I	L	A	H	I	H	Y	M	P	449
ATG	GTG	TTC	TGC	CCT	GAG	CAG	CTG	CTC	CGC	GTG	ATC	CTC	GCT	CAC	ATC	CAC	TAC	ATG	CCT	1466

**Fig. 17J**

D	H	W	Q	G	N	A	H	R	S	Q	T	R	D	E	F	A	Q	L	F	469
GAC	CAC	TGG	CAG	GGT	AAT	GCC	CAC	CGC	TCG	CAG	ACC	CGG	GAC	GAG	TTT	GCC	CAG	CTC	TTC	1526
Q	Y	K	A	V	F	I	L	E	E	L	L	S	P	I	V	T	P	L	I	489
CAG	TAC	AAG	GCA	GTG	TTC	ATT	TTG	GAA	GAG	TTG	CTG	AGC	CCC	ATT	GTC	ACA	CCC	CTC	ATC	1586
L	I	F	C	L	R	P	R	A	L	E	I	I	D	F	F	R	N	F	T	509
CTC	ATC	TTC	TGC	CTG	CGC	CCA	CGG	GCC	CTG	GAG	ATT	ATA	GAC	TTC	TTC	CGA	AAC	TTC	ACC	1646
V	E	V	V	G	V	G	D	T	C	S	F	A	Q	M	D	V	R	Q	H	529
GTG	GAG	GTC	GTT	GGT	GTG	GGA	GAT	ACC	TGC	TCC	TTT	GCT	CAG	ATG	GAT	GTT	CGC	CAG	CAT	1706
G	H	P	Q	W	L	S	A	G	Q	T	E	A	S	V	Y	Q	Q	A	E	549
GGT	CAT	CCC	CAG	TGG	CTA	TCT	GCT	GGT	CAG	ACA	GAG	GCC	TCA	GTG	TAC	CAG	CAA	GCT	GAG	1766
D	G	K	T	E	L	S	L	M	H	F	A	I	T	N	P	G	W	Q	P	569
GAT	GGA	AAG	ACA	GAG	TTG	TCA	CTC	ATG	CAC	TTT	GCC	ATC	ACC	AAC	CCT	GGC	TGG	CAG	CCA	1826
P	R	E	S	T	A	F	L	G	F	L	K	E	Q	V	Q	R	D	G	A	589
CCA	CGT	GAG	AGC	ACA	GCC	TTC	CTA	GGC	TTC	CTC	AAG	GAG	CAG	GTT	CAG	CGG	GAT	GGA	GCA	1886
A	A	S	L	A	Q	G	G	L	L	P	E	N	A	L	F	T	S	I	Q	609
GCT	GCT	AGC	CTC	GCC	CAA	GGG	GGT	CTG	CTC	CCT	GAA	AAT	GCC	CTC	TTT	ACG	TCT	ATC	CAG	1946

**Fig. 17K**

S	L	Q	S	E	S	E	S	P	L	S	L	I	A	N	V	V	A	G	S	S	629
TCC	TTA	CAA	TCT	GAG	TCT	GAG	CCC	CTG	CTG	AGC	CTT	ATC	GCA	AAT	GTG	GTA	GCT	GGC	TCA	TCC	2006
C	R	G	P	P	L	P	R	R	D	L	Q	G	S	R	R	A	H	S	T	M	649
TGC	CGG	GGC	CCT	CCA	CTG	CCC	AGA	GAC	CTG	CAG	GGC	TCC	AGG	CGG	GCT	CAC	AGC	ACC	ATG	2066	
T	G	S	G	V	D	A	R	T	A	S	S	S	G	S	S	V	W	E	G	Q	669
ACA	GGC	TCT	GGG	GTG	GAT	GCC	AGG	ACA	GCC	AGC	TCC	GGG	AGC	AGC	AGC	GTG	TGG	GAA	GGA	CAG	2126
L	Q	S	L	V	L	S	E	Y	A	S	T	E	M	S	S	L	H	A	L	Y	689
CTG	CAG	AGC	CTG	GTG	CTG	TCA	GAA	TAT	GCA	TCC	ACA	GAG	ATG	AGC	CTG	CAT	GCC	CTC	TAT	2186	
M	H	Q	L	H	K	Q	Q	A	Q	A	E	P	E	R	H	V	W	H	R		709
ATG	CAC	CAG	CTC	CAC	AAG	CAG	CAG	GCC	CAG	GCT	GAA	CCT	GAG	CGG	CAT	GTA	TGG	CAC	CGC	2246	
R	E	S	D	E	S	G	E	S	A	P	D	E	G	G	E	G	A	R	A		729
CGG	GAG	AGT	GAT	GAG	AGT	GGA	GAA	AGC	GCC	CCT	GAT	GAA	GGG	GGA	GAG	GGC	GCC	CGG	GCC	2306	
P	Q	S	I	P	R	S	A	S	Y	P	C	A	A	P	R	P	G	A	P		749
CCC	CAG	TCT	ATC	CCT	CGC	TCT	GCT	AGC	TAT	CCC	TGT	GCA	GCA	CCC	CGG	CCT	GGA	GCT	CCT	2366	
E	T	T	A	L	H	G	G	F	Q	R	R	Y	G	G	I	T	D	P	G		769
GAG	ACC	ACC	GCC	CTG	CAT	GGG	GGC	TTC	CAG	AGG	CGC	TAC	GGT	GGC	ATC	ACA	GAT	CCT	GGC	2426	

**Fig. 17L**

T	V	P	P	R	V	P	S	H	F	S	R	L	P	L	G	G	W	A	E	D	789
ACA	GTG	CCC	AGG	GTT	CCC	TCT	CAT	TTC	TCT	CGG	CTG	CCT	CTT	GGA	GGG	TGG	GCA	GAA	GAT	2486	
G	Q	S	A	S	R	H	P	P	E	P	V	P	E	E	G	S	E	D	E	L	809
GGG	CAG	TCG	GCA	TCA	AGG	CAC	CCT	GAG	CCC	GTG	CCC	GAA	GAG	GGC	TCG	GAG	GAT	GAG	GAT	2546	
P	P	Q	V	H	K	V	*													817	
CCC	CCT	CAG	GTG	CAC	AAG	GTA	TAG													2570	
ACA	AGG	CTG	AGC	AGG	TTT	CTG	TGG	CCC	AGG	ATG	GAG	CCG	CTG	CCC	TGCC	ATC	CCCG	TCT	GCCT	GGG	2649
CTC	CTC	TG	AGT	GT	TCC	CTG	GGC	CCC	ACG	TTG	TGT	GT	CT	TGT	CTG	CTG	CCCA	AGG	AGT	GCA	2728
TTG	CCAC	AGC	CCC	CAG	GAG	AGG	AAT	TTG	GGC	CTAG	GAAC	CGG	CAC	ACG	GACT	CTAG	CCCT	ATC	CCCC	AGG	2807
TTG	GCT	CAG	AGT	GTG	TGCT	AG	AACT	GGT	CCCC	AGC	CCCA	GTACT	GCC	ACCT	TTAC	ACCT	ACCT	ACCT	ACCT	GCA	2886
CCC	AG	GGCT	GCCC	ACG	ATAG	AAG	CTGCC	AAG	CAG	GAAC	CTGT	GCC	AAC	TGT	GAG	TGG	GAG	GT	GGC	CTG	2965
CCCT	CA	ACCC	CTG	CA	ACCT	TCC	CTAG	CCCC	CTCA	ATAG	ATG	AGC	AGT	CAG	GTG	GCCC	TTAC	CT	ACCC	GAG	3044
TCG	CCC	AGT	GC	AGC	CGG	CTC	AC	CTC	TCC	GTCT	CTT	TG	CA	CTC	AC	TG	GT	GT	GT	CTC	3123
GT	TCG	CT	TG	CTC	CGT	TC	CGG	CTT	TG	CGT	TTG	CGT	TAG	GGT	GA	AGC	CTAG	CGT	CCCT	CA	3202
ATTT	TG	AC	ACT	AA	AA	AGG	TTT	CT	AA	ATT	G	AGC	AGG	ATG	GA	AA	TACT	TTG	CTC	CTT	3281
TGG	CCCC	CC	AGG	AG	ACT	GT	CT	TCC	TGG	CCC	TC	AT	TG	CTG	CTT	AT	CGT	AC	CCCC	ATC	3360
CCG	GGCT	GG	AGG	TG	AC	CT	TGG	CTGT	AC	GT	CC	CAG	CA	AA	AG	AG	CTC	TG	CCCC	GC	3439
ATGA	AGG	CGG	AT	GC	CT	CG	CCG	AGG	CTT	TGG	GT	GG	CTG	CTG	CA	TG	CTG	GG	ACT	CTC	3518
CAC	CC	AG	CT	GT	GT	CGG	CTT	TGG	AG	AGT	GT	GA	ATT	CG	CT	G	CCG	AA	CTC	G	3597
AC	AG	CT	TG	ATA	AC	CTT	ATA	ATA	AA	AGG	AGT	TTG	AC	CA	GA	AAAA	AAAA	AAAA	AAAA	AAAA	3674

Fig. 17M

GCTGGAGCGGAGCGCAGGCAATGCTCAGCCCTGGATGTAGCTGAGAGGCTGGGAGAAAGACGACCGCTGGAGACCG	79
ACCGCGTGGGGAAGACCTAGGGGGTGGTGGGGAAGCAGACAGGAGAACAACCTCGAAATCAAGCGCTTTACAGATTA	158
TTTTATTTTGTATAGAGAAACACGTAGCGACTCCGAAGATCAGCCCCA ATG AAC ATG TCA GTG TTG ACT TTA	229
Q E Y E F E K Q F N E N E A I Q W M Q E	28
CAA GAA TAT GAA TTC GAA AAG CAG TTC AAC GAG AAT GAA GCC ATC CAA TGG ATG CAG GAA	289
N W K K S F L F S A L Y A A F I F G G R	48
AAC TGG AAG AAA TCT TTC CTG TTT TCT GCT TAT GCT GCC TTT ATA TTC GGT GGT CGG	349
H L M N K R A K F E L R K P L V L W S L	68
CAC CTA ATG AAT AAA CGA GCA AAG TTT GAA CTG AGG AAG CCA TTA GTG CTC TGG TCT CTG	409
T L A V F S I F G A L R T G A Y M V Y I	88
ACC CTT GCA GTC TTC AGT ATA TTC GGT GCT CTT CGA ACT GGT GCT TAT ATG GTG TAC ATT	469
L M T K G L K Q S V C D Q G F Y N G P V	108
TTG ATG ACC AAA GGC CTG AAG CAG TCA GTT TGT GAC CAG GGT TTT TAC AAT GGA CCT GTC	529
S K F W A Y A F V L S K A P E L G D T I	128
AGC AAA TTC TGG GCT TAT GCA TTT GTG CTA AGC AAA GCA CCC GAA CTA GGA GAT ACA ATA	589

**Fig. 18A**

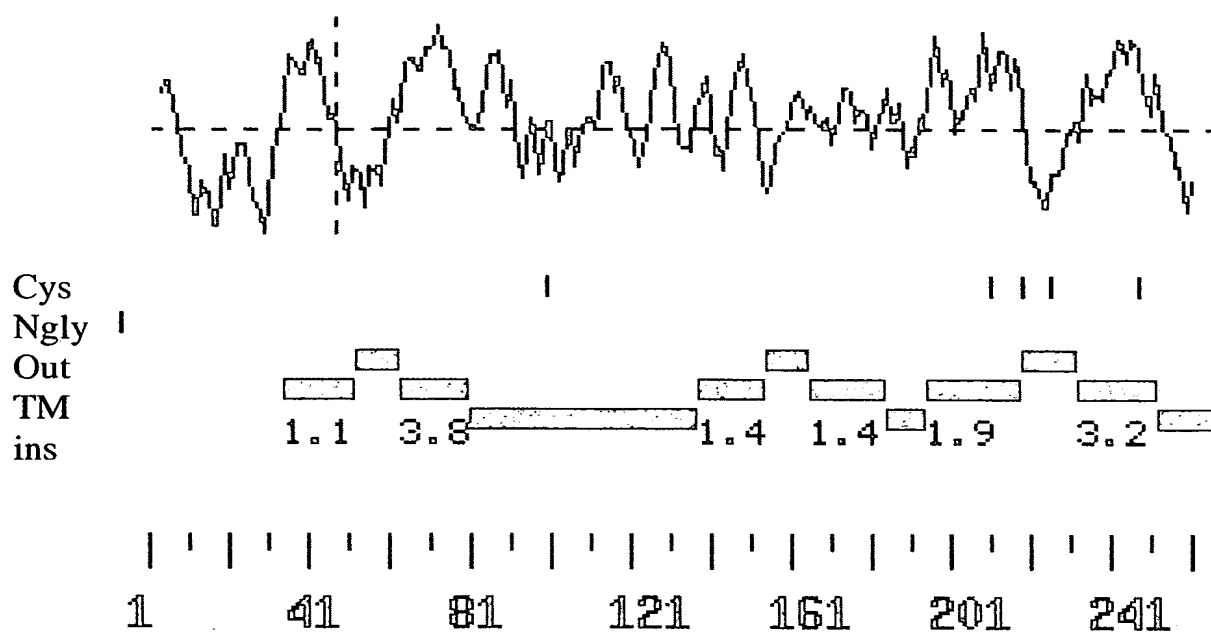


F	I	I	L	R	K	Q	K	L	I	F	L	H	Y	H	H	I	T	V	148	
TTC	ATT	ATT	CTG	AGG	AAG	CAG	AAG	CTG	ATC	TTC	CTG	CAC	TGG	TAT	CAC	ATC	ACT	GTG	649	
L	L	Y	S	W	Y	S	Y	K	D	M	V	A	G	G	W	F	M	T	168	
CTC	CTG	TAC	TCT	TGG	TAC	TCC	TAC	TAC	AAA	GAC	ATG	GCC	GGG	GGA	GGT	TTC	ATG	ACT	709	
M	N	Y	G	V	H	A	V	M	Y	S	Y	Y	A	L	R	A	A	G	F	188
ATG	AAC	TAT	GGC	GTG	CAC	GCC	GTG	ATG	TAC	TCT	TAC	TAT	TAT	GCC	CGG	GCA	GGT	TTC	769	
R	V	S	R	K	F	A	M	F	I	T	L	S	Q	I	T	Q	M	L	M	208
CGA	GTC	TCC	CGG	AAG	TTT	GCC	ATG	TTC	ATC	ACC	TTG	TCC	CAG	ATC	ACT	CAG	ATG	CTG	ATG	829
G	C	V	V	N	Y	L	V	F	C	W	M	Q	H	D	Q	C	H	S	H	228
GGC	TGT	GTG	GTT	AAC	TAC	CTG	GTC	TTC	TGC	TGG	ATG	CAG	CAT	GAC	CAG	TGT	CAC	TCT	CAC	889
F	Q	N	I	F	W	S	S	L	M	Y	L	S	Y	L	V	L	F	C	H	248
TTT	CAG	AAC	ATC	TTC	TGG	TCC	TCA	CTC	ATG	TAC	CTC	AGC	TAC	CTT	GTG	CTC	TTC	TGC	CAT	949
F	F	F	E	A	Y	I	G	K	M	R	K	T	T	K	A	E	*			266
TTC	TTC	TTT	GAG	GCC	TAC	ATC	GGC	AAA	ATG	AGG	AAA	ACA	ACG	AAA	GCT	GAA	TAG			1003
TGTTGGA	ACTGAGG	AGCCATAGCTCAGGGT	CATCAAGAAA	AATAATAGACAAA	AGAAAATGGCACA	AGGAATCAC	1082													
ACGTGGT	GCGCTAAA	ACAAAACATGAGCA	AAACACAAAACCC	AAGCAGCTTAGG	GATAATTAGGTTGATT	TAA	1161													

Fig. 18B

CCCAGTAAGTTTATGATCCTTTTAGGGTGAGGACTCACTGAGTGCACCTCCATCTCCAAGCACCTGCTGCTGGAAGACCC 1240  
 CATCCCTCTTTTATCTATCAACTCTAGGACAAAGGAGAACAAAGCAAGCCAGAACGAGAGAGACTAATCAAAAGGCAA 1319  
 ACAAGGCTATTAAACACATAGGAAAAAATGTATTACTAAGTGTACATTTCTCTAAGATGAAAATTTTACTCTAGA 1398  
 AACTGTGCGAGCAACAACACACAATCCTTTCTAACTTATGGACACTAAACTGGAGCCAAATAGAAAAAGACAAAAATGA 1477  
 AAGAGACACAGGGTGATATCTAGAACGATAATGCTTTTGCAGAAACTAAAGCCTTTTAAAGAAATGCCAGCTGCTGTA 1556  
 GACCCCATGAGAAAAAGATGTCTTAATCATCCTTATGAAAAACAGATGTAAACAACATAATTTCAAACCTCACTCTTCA 1635  
 CTGCATAGCCTCAGGCTAGTGAGTTTGCCAAAACCAAGGGGTGAATACTTCCCCAAGATTCTTCCCTGGGAGGATGGA 1714  
 AACAGTGCAGCCAGGTCCTCAGGGGAGCTCCATCCAGAGCATTTCTGTATAGTTGAACCTGTAATTTCTACTCTTAA 1793  
 GTGAGATATGAAGCATTAATCCTTTTGTTCAGTTGCCCGGGCTTTTGAAACAGAAAGATAAATACAGAAATTGAAAAAGAT 1872  
 AAACACTCAACCAACAATGTGAAAAACGGGTTCTGTAGTATTGTAAAAAGGCCCGGCCAGGACCACTGTGAGCTGGA 1951  
 AAAGGGAGAAAGGCAGTGGGAAAAGAGGTGAGCCGAAGATCAATTCGACAGACAGACGGTGTGTATGCCCTCCCTGTT 2030  
 TGACTTCACACACACTCAATACTTTCCAAATGAAACCCACAGTATAGCGCATATTTTCGATATTTTGTGAAATTCCAA 2109  
 AAGGAAATCACAGGGCTGTTTCGAAATATTGGGGAACACTGTGTTTCTGCATCATCTGCATTTGCTCCCCAAGCAATGT 2188  
 AGAGGTGTTTAAAGGGCCCTCTGCTGGCTGAGTGGCAATACTACAACAACCTCAAGGCAAGTTTGGCTGAAAAACAGTT 2267  
 GACAACAAGGGCCCCCATACACTTATCCCTCAAAATTTTAAGTGATATGAAATACCTTGTCATGCTTTGGCCAAATCAG 2346  
 AAGATATTCAATCCTGCTTCAAGTCAGCTTCAGAAATGTTTAAAGGGACTTTAGCTCTGGAACCTCAAAATCAATTTAT 2425  
 TAAGAGCCATATTCTTTAAAAAAAAGCTGGATAATAATTCCTGTAAATATTTTCAGTCCTTTACAAAGCCAAATACATG 2504  
 TGTCAATGTTTCTAGTATTTCAAAGAAAGCAATATGTAAAGTTGTTCAATGTGACATAATAGTATTAATAATTGGTTAAG 2583  
 TAGCTTAATGATTAGGCAAACTAGATGAAAAGATTAGGGGCTTCCACACTGCATAGATTACACGCACATAGCCACGCAT 2662  
 ACACACACAGACACAGATGTGGGTACACTGAACTTCAAGCCCCAAATGAATAGAAACACATTTTCTGGCTAGCAGA 2741  
 AAAAAACAAAACAAAACCTGTGTTTCTCTTCTTCTGCTTTGAGAGTGTACAGTAAAAGGATTTTTCGAAATTAATTTTA 2820  
 TATTATTTTAGCTTTAATTGTGCTGCTGTTCAATGAAACAGAGCTGCTCTGCTTTTCTGTCAAGAGATGGCAAGGCTTTT 2899  
 TCAGCATCTCGTTTATGTGTGGAATTTAAAAAGAAATAAAGTTTATTCCATTCTGTGTGAAAAAATAAAAAA 2978  
 AAAAAAATAAAAAA 2989

Fig. 18C



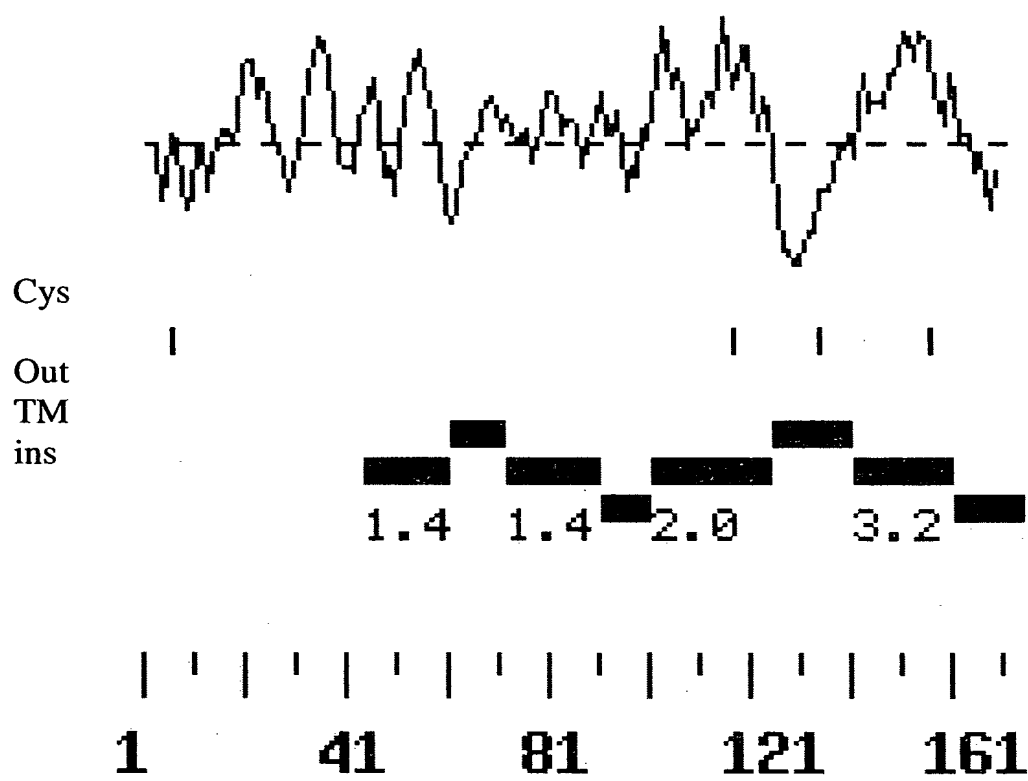
**Fig. 18D**

L	K	Q	S	V	C	D	Q	S	F	Y	N	G	P	V	S	K	F	W	19	
GC	CTG	AAG	CAG	TCA	GTT	TGT	GAC	CAG	AGT	TTT	TAC	AAT	GGA	CCT	GTC	AGC	AAA	TTC	TGG	59
A	Y	A	F	V	L	S	K	A	P	E	L	G	D	T	I	F	I	I	L	39
GCT	TAT	GCA	TTT	GTG	CTC	AGC	AAA	GCA	CCC	GAA	CTA	GGT	GAC	ACG	ATA	TTC	ATC	ATT	CTG	119
R	K	Q	K	L	I	F	L	H	W	Y	H	H	I	T	V	L	L	Y	S	59
AGG	AAA	CAG	AAA	CTG	ATC	TTC	CTG	CAC	TGG	TAC	CAC	CAC	ATC	ACT	GTG	CTC	CTG	TAC	TCC	179
W	Y	S	Y	K	D	M	V	A	G	G	G	W	F	M	T	M	N	Y	G	79
TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTC	GCT	GGG	GGT	GGT	TGG	TTC	ATG	ACT	ATG	AAC	TAT	GGC	239
V	H	A	V	M	Y	S	Y	Y	A	L	R	A	A	G	F	R	V	S	R	99
GTG	CAT	GCC	GTC	ATG	TAC	TCT	TAC	TAC	GCC	TTG	CGG	GCT	GCG	GGT	TTC	CGA	GTC	TCC	CGG	299
K	F	A	M	F	I	T	L	S	Q	I	T	Q	M	L	M	G	C	V	I	119
AAG	TTT	GCC	ATG	TTC	ATC	ACC	TTG	TCC	CAG	ATC	ACT	CAG	ATG	CTG	ATG	GGC	TGT	GTC	ATT	359
N	Y	L	V	F	N	W	M	Q	H	D	N	D	Q	C	Y	S	H	F	Q	139
AAC	TAC	CTG	GTC	TTC	AAC	TGG	ATG	CAG	CAT	GAC	AAC	GAC	CAG	TGC	TAC	TCC	CAC	TTT	CAG	419
N	I	F	W	S	S	L	M	Y	L	S	Y	L	V	L	F	C	H	F	F	159
AAC	ATC	TTC	TGG	TCC	TCG	CTC	ATG	TAC	CTC	AGC	TAC	CTT	GTG	CTC	TTC	TGC	CAT	TTC	TTC	479

Fig. 18E

F	E	A	Y	I	G	K	V	K	K	A	T	K	A	E	*	175
TTT	GAG	GCC	TAC	ATC	GGC	AAA	GTG	AAG	AAA	GCC	ACG	AAG	GCT	GAG	TAG	527
TGTCAGGGCTGAGGAGGAAGTCATAGCTCAGGGTCATCAGGAAAAATAATCGACAAAAAATGGCACAAAGGAATCC	606															
CATATGGTGCAGCTAAACAAACAAACATCCGTAATGAGCAGGCACGAGGCCCAAGGCAGCTTGGGACTGAAGATTAG	685															
GTTGTAAGTTTATGATCCCTTTCTGGTGAGGACTCGCTGAGTGCAACTCTTATCTCAAAGCACGGCTGCTGAGGGGACC	764															
CCTTCCCTCTGGCCTGTCAACTCTAGAACACACATAGATGCAAAAGGCAGCCACGGGCAAGAGATTGGGCAGAGATTAGT	843															
GGACGGCCAGCAAAACACTGCAGGAAAGCAGGTGGGGGAGGAATCTACTCAGCCTTTGTGTTTGTGTTTGTGTTT	922															
GTTTTTCTCTAAGGATAAAGGAGTTTCCCTTTTCAACGATGTGAGCACACACACACACACACACACACACACA	1001															
CACACACACACGCAATCTTTTCAACACGAAACCCAGAGCTAAAAGAAAAGATAAACATGGGAGAGACAGGGTTTCTAT	1080															
CTGGGACAGCAATGCTTTTGCAAAAGGCTAGGCCTTTAAAGAAAAGGTGAGCTTGTAACTCCTTGATAAAAGATGTCTT	1159															
AATTATTTTACTGCAACTGAAAGTAAAGAGGTAGAGCCTTTCCCTTCTGCACAGCCTCAGGGCTTGATGTCTCTA	1238															
CAACCAACACACAGGACAGTACTTCCCCCATGATACTTTATTACTGGGAGAAAAGAAACCCCTGTAGTTGAAACACCCAC	1317															
TGACAACTGTATTCTGCTCTCCGACGAGAAATTCAGCATCCGTTGTTTCAGTTGCCCAAACCTTTAGGACGGAGGAGT	1396															
AAATGCAGAACTGAAAGGGAAGAGCTCAGCTGGCTGGCTTGAAAATGGAGTCTTGTAACCATGTGTAACAAATGCCAGC	1475															
CCATCGTCCCTGGAGCTGAACAGGGAGGAGGCTATGGGCAGAGACTAGAGCCGGATTCAATCCAAATGTGCAGACAGCG	1554															
TGTTCGCCTCCCTCCCTGTTTCGACCTCACACATAATCCTGGCTTCTAAATGAGGCCCTGTGACACACTCTGTGCTTTC	1633															
TATATTTTGTGACTTTCAACACAGATCTGCAGGGCTCTGCCCTGATTTGGGGTAAACACTGTGTTTCTGCAGCCCTCG	1712															
CATTGCTCCCTTCAGCAGTGCAGAGGCTTGAGAAAGTGCCCTCTGCTGGCTTAGTGAGAAAGCTTCAACAAACACTTCAC	1791															
AGTAGGTTGAAAATAACTGACCCTAAGGGCTGCGGAGATTAAACCCTAAGTTCTAAGTGTCTCAAAACACCTGACATA	1870															
TATTTGACCAAAATCAGAAAGAGAGAGAAACCTCTATGCTTCAAGTAAGCGTCAATAAATTTTAAAGTGACTTTCACCTG	1949															
AGAACTCAGAAAGTCAATGTATTAAAGAGCCATATTCTGAAAGAAAAGAGAAAAGAGAAAAGAAAAA	2028															
AAAA	2032															

**Fig. 18F**



**Fig. 18G**



human	ATGAACATGTCAGTGTGACTTTACAAAGAAATATGAATTCGAAAAGCAGTTCAACGAGAAATGAAGCCATCC	10	20	30	40	50	60	70
murine	-----							
human	AATGGATGCAGGAAAACCTGGAAGAAATCTTCCCTGTTTCTGCTCTGTATGCTGCCCTTTATATTCGGTGG	80	90	100	110	120	130	140
murine	-----							
human	TCGGCACCTAATGAATAAACGAGCAAAGTTTGAACCTGAGGAAGCCATTAGTGCTCTGGTCTCTGACCCCTT	150	160	170	180	190	200	210
murine	-----							
human	GCAGTCTTCAGTATATTCGGTGCTCTTCGAACTGGTGCTTATATGGTGACATTTTGATGACCAAAGGCC	220	230	240	250	260	270	280
murine	-----							

**Fig. 18I**



human	290	300	310	320	330	340	350
	TGAAGCAGTCAGTTTGTGACCAAGGGTTT	TACAAATGGACCTGTCAGCAAAT	TCTGGGCTTATGCATTGT				
murine	10	20	30	40	50	60	70
	TGAAGCAGTCAGTTTGTGACCAAGAGTTT	TACAAATGGACCTGTCAGCAAAT	TCTGGGCTTATGCATTGT				
human	360	370	380	390	400	410	420
	GCTAAGCAAGCACCCGAACTAGGAGATACA	ATATTCAATTATCTGAGGAAGCAGAACTG	ATCTTCCTG				
murine	80	90	100	110	120	130	140
	GCTCAGCAAAGCACCCGAACTAGGTGACAC	GCATATTCATCATCTCTGAGGAAACAGAA	ACTGATCTTCCTG				
human	430	440	450	460	470	480	490
	CAC	TGGTATCACCACATC	ACTGTGCTCCTGTACTCTTGGTACTCCT	TACAAAGACATGGTTGCCGGGGAG			
murine	150	160	170	180	190	200	210
	CAC	TGGTACCACACATC	ACTGTGCTCCTGTACTCCTCTGCTACTCCT	TACAAAGACATGGTCTGCTGGGGTG			
human	500	510	520	530	540	550	560
	GTTGGTTCA	TGACTATGA	ACTATGGCGTGCACGCCG	TGATGTACTCTTACTATGCCCTTGCCGGGGCAGG			
murine	220	230	240	250	260	270	280
	GTTGGTTCA	TGACTATGA	ACTATGGCGTGCATGCCG	TGATGTACTCTTACTACGCCCTTGCCGGGTGCGGG			

**Fig. 18J**

human	570	580	590	600	610	620	630
	TTTCCGAGTCTCCCGAAGTTTGCCATGTTTCATCACCTTGTC	CCAGATCACTCAGATGCTGATGGGCTGT					
murine	290	300	310	320	330	340	350
	TTTCCGAGTCTCCCGAAGTTTGCCATGTTTCATCACCTTGTC	CCAGATCACTCAGATGCTGATGGGCTGT					
human	640	650	660	670	680	690	
	GTGGTTAACTACCTGGTCTTCTGCTGGATGCAGCATGAC----	CAGTGTCACTCTCACTTTCAGAAACA					
murine	360	370	380	390	400	410	420
	GTCATTAACTACCTGGTCTTCAACTGGATGCAGCATGACAACGAC	CGTGTCTACTCCCACCTTTCAGAAACA					
human	700	710	720	730	740	750	760
	TCTTCTGGTCCCTCACTCATGTACCTCAGCTACCTTGTCCTCTTCTG	CCATTCTTCTTGAGGCCTACAT					
murine	430	440	450	460	470	480	490
	TCTTCTGGTCCCTCGCTCATGTACCTCAGCTACCTTGTCCTCTTCTG	CCATTCTTCTTGAGGCCTACAT					
human	770	780	790				
	CGGCAAAATGAGGAAAACAACGAAAGCTGAA						
murine	500	510	520				
	CGGCAAAAGTGAAGAAAGCCACGAAAGCTGAG						

**Fig. 18K**

```
I400 MDTSMNFSRGLKMDLMQPYDFET-FQDLRPF--LEEYWVSSFLIVVVYLLLVVGQTYMRTRKSFSLSLQR  
: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
CIG30 MNMSV-----LTL---QEYEFEKEQNENEAIQMOMENWKKSFIFSALYAAFIFGGRHLMNKRAKFELRK  
10      20      30      40      50      60  
70      80      90      100     110     120     130  
I400 LILWSFFLAIFSILGTLRMWKFMATVMFTVGLKQTVCFAIYTDDAVRFWSFLFLSKVVVELGDTAFIIL  
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
CIG30 LVLWSLT LAVSIFGALRTGAYMVVIILMTKGLKQSVCDQGFYNGPVS KFWAYAFVLSKAPELGDTIFIIL  
70      80      90      100     110     120     130  
140      150     160     170     180     190     200  
I400 RKRPLIFVHWYHHSTVLLFTSFGYKNKVPSGGWFMTMNFVHSVMYTYTMMKAAKLKHPNLLPMVITSLQ  
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
CIG30 RKQKLIFLHWYHHITVLLYSWYSYKDMVAGGGWFMTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSQ  
140      150     160     170     180     190     200  
210      220     230     240     250     260     270  
I400 ILQMVLGTIFGILNIWRQEKGCHTTTEHFFWSFMLYGTYFILFAHFFHRAYLPRPGKVASKSQ  
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
CIG30 ITQMLMGCVVNVLVFCWMQHDQCHSHFQNI FWS SLMYLSVLVLFCHFFEAYI-GKMRKTTKAE  
210      220     230     240     250     260
```

**Fig. 18L**

```

10      20      30      40      50      60
I400 ATGAACATGTCAGTGTGACTTTACAAGAAATATGAATT--CGAAAAAGCAGTTTCAACGAGAAATGAAGC--
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CIG30 ATGGACACATCCCATGAATTTCTCACGCGGGTTAAAAAATGGACCTTGATGCAACCCCTATGACTTCGAGACGT
      10      20      30      40      50      60      70

      70      80      90      100      110      120
I400 --CA--TCCAATGG-----ATGCAGGAAAACTGGAAGAAATCTTTCCCT-GTTTCTTCTGC-TCTGTATGCT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CIG30 TTCAGGACTTAAGGCCCTTTTGGAGGAGTACTGGGTAAGCTCATTTCTCATAGTGGTCTCTATCTGTT
      80      90      100      110      120      130      140

      130      140      150      160      170      180      190
I400 GCCTTTATATTTCGGTGGTCGGCACCTA-ATGAATAAACGAGCAAAAGTTTGAAC-T-GAGGAAGCCATTAGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CIG30 GC--TCATCGTTGTTGGCCAG-ACCTACATGAGAACGCCGA-AGAGCTTCAGCTTGCAGAGGCCCTCTCAT
      150      160      170      180      190      200

      200      210      220      230      240      250      260
I400 GCTCTGGTCTCTGACCCCTTGACGTCTTCAGTATATTCGGTGCTCTTCGAACTGGTGTCTTATATGGTGAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CIG30 CCTCTGGTCCCTTCTTCCCTGGCAATATTCAGTATCCTGGGTACTCTGAGGATGTGGAAGTTTATGGCAACA
      210      220      230      240      250      260      270

```

**Fig. 18M**

[illegible]

**Fig. 18N**

```

540      550      560      570      580      590      600
I400 TACTATGCCCTTGC GCGGCAGGTTTCCGAGTCTCCCGAAGTTTGCC--ATGTTTCATCACCTTGTCC--
      ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . .
CIG30 TACTACACTATGAAGGCTGCCAAA--CTGAAGCATCCCTAATCTTCTCCCCCATGGTTCATCACCAG--CCTG
      560      570      580      590      600      610

610      620      630      640      650      660      670
I400 CAGATCACT-CAGATGCTGATGGGCTGTGTGGTTAACTACCTGGTCTTCTGCTGGATGCAGCATGACCAG
      ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . .
CIG30 CAGAT-TCTGCAGATGGTTCTGGGCACCATCTTTGGCATACTGAATTACATCTGGAGGCAGGAGAAAAGGA
      620      630      640      650      660      670      680

680      690      700      710      720      730      740
I400 TGTCACTCTCACTTTTCAGAAACA--TCTTCTGGTCCCTCACTCATGTACCTCAGCTACCTTGTGCTCTTCTG
      ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . .
CIG30 TGCCACACA-ACAA-CGGAACACTTCTTCTGGTCTTTTATGCTATATGGACCTATTTTCATCCTATTTCGC
      690      700      710      720      730      740      750

750      760      770      780      790
I400 CCATTTCTTCTTTGAGGCCCTACATCGG--CAAAATGAGGAAAAACAAC-GAAAGCTGAA
      ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . . ::::: . . . . .
CIG30 TCAC TTCTTCCACCGAGCCTACCTCAGGCCCAAGGCAAAAGTTGCATCCAAGAGCC-AA
      760      770      780      790      800      810

```

**Fig. 180**

L	G	D	T	I	F	I	I	L	R	K	Q	K	L	I	F	L	H	W	Y	20
CTA	GGT	GAT	ACG	ATA	TTC	ATC	ATT	CTG	AGG	AAG	CAG	AAG	CTG	ATC	TTC	CTG	CAC	TGG	TAC	60
H	H	I	T	V	L	L	Y	S	W	Y	S	Y	K	D	M	V	A	G	G	40
CAC	CAC	ATC	ACT	GTG	CTC	CTG	TAC	TCT	TGG	TAC	TCC	TAC	AAA	GAC	ATG	GTA	GCT	GGG	GGT	120
G	W	F	M	T	M	N	Y	G	V	H	A	V	M	Y	S	Y	Y	A	L	60
GGT	TGG	TTC	ATG	ACT	ATG	AAC	TAT	GGC	GTA	CAC	GCC	GTC	ATG	TAC	TCT	TAC	TAC	GCC	TTG	180
R	A	A	G	F	R	V	S	R	K	F	A	M	F	I	T	L	S	Q	I	80
CGG	GCT	GCG	GGT	TTC	CGG	GTC	TCC	CGG	AAG	TTT	GCC	ATG	TTC	ATC	ACG	TTG	TCC	CAG	ATC	240
T	Q	M	L	M	G	C	V	I	N	Y	L	V	F	N	W	M	Q	H	D	100
ACT	CAG	ATG	CTG	ATG	GGC	TGT	GTC	ATT	AAC	TAC	CTG	GTC	TTC	AAC	TGG	ATG	CAG	CAT	GAC	300
N	D	Q	C	Y	S	H	F	Q	N	I	F	W	S	S	L	M	Y	L	S	120
AAT	GAC	CAG	TGC	TAC	TCC	CAC	TTT	CAG	AAC	ATC	TTC	TGG	TCC	TCA	CTC	ATG	TAC	CTC	AGC	360
Y	L	L	L	F	C	H	F	F	F	E	A	Y	I	G	K	V	K	K	A	140
TAC	CTT	CTG	CTC	TTC	TGC	CAT	TTC	TTC	TTT	GAG	GCC	TAC	ATC	GGC	AAA	GTG	AAG	AAA	GCG	420
T	K	A	E	*																145
ACG	AAG	GCC	GAG	TAG																435

**Fig. 18P**

TGTCAGAGCTGAGGAGGAAAGACATAGCTCAGGGTCATCACGAAAAAATAATAGACAAAAAAGAAAAATGGCACACAAGGAATCA 514  
CATATGGTGCAGCTAAACAAAAACAACATTATGAGCAGACGCTAAGCCCCAAGCAGCTTGGGAGTGAAGATTAGGTT 593  
GTAAGTTTATGATCCCTTTTGGGTGAGGACTCACTGAGAACACTGCTGCTGAGGACCCCTTCCCTCTTACCTGTCAA 672  
CTCTAGAACACACTAGAAGCCAAAGGCAGCCATGGGCAAGGAGATTAGTGGACAGCAAGCAAAACACTGCAGGAAGAGGG 751  
GGGAGATCTATTTCAGAGTTTGTGTTTGTGTTTGTGTTTGTGTTTCTCTAAGGATAAAGGAGTTTCCCCCTTTTCAAACTG 830  
TGTGAGCACACCCACGCGCATGCAGACACACCCACCTACACACTATCTGCAGATGACCAAGTGTCTATGCTGTTTTTTAC 909  
AAATAAACTTGAGACAAGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA 974

**Fig. 18Q**



	10	20	30	40	50	60	70	
human	MNMSVLT	LQEYEF	EKFQFN	ENEAIQ	WMQEN	WKKSFL	SALYA	AAFIFG
murine	-----	-----	-----	-----	-----	-----	-----	-----
rat	-----	-----	-----	-----	-----	-----	-----	-----
human	AVFSIF	GALRT	GAYMV	YILMT	KGLKQ	SVCDQ	GFYNG	PVSKF
murine	-----	-----	-----	-----	-----	-----	-----	-----
rat	-----	-----	-----	-----	-----	-----	-----	-----
human	HWYHHI	TVLLY	SWYSY	KDMV	AGGGW	FMTMN	YGVH	AVMYS
murine	-----	-----	-----	-----	-----	-----	-----	-----
rat	-----	-----	-----	-----	-----	-----	-----	-----
human	VVNYLV	FCWMQ	HD--Q	CHSHF	QNI	FWSSL	MYLSY	LVLF
murine	-----	-----	-----	-----	-----	-----	-----	-----
rat	-----	-----	-----	-----	-----	-----	-----	-----

Fig. 18R

GTCCACCCACGGTCCGGGGAGCGGGCTAAGAGTGCCGCACCGCCTCACAACCTGGGAACCGGAGAGTAGGGGCCGTC	79
GGCTGGCAAGAACCCGCGTGCCCTCCTCGGCAAGGGCCATCCGGTGCCACCCCATGTGCGCACTAGAGCAGAAGAGGGTGA	158
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> <span>M</span><span>T</span><span>W</span><span>L</span><span>V</span> </div> GTCCCTGAACCTGCAACCTGCACAGAGCTGCTCTGTACTGTCCCTGGTGGTGGCCGCC ATG ACC TGG TTG GTG	5 229
L L G T L L C M L R V G L G T P D S E G CTG CTG GGG ACA CTG CTC TGC ATG CTG CGC GTT GGG TTA GGC ACC CCG GAC TCC GAG GGT	25 289
F P P R A L H N C P Y K C I C A A D L L TTC CCG CCC CGT GCG CTC CAC AAC TGC CCC TAC AAA TGT ATC TGC GCT GCC GAC CTG CTA	45 349
S C T G L G L Q D V P A E L P A A T A D AGC TGC ACT GGC CTA GGG CTG CAG GAC GTG CCA GCC GAG TTA CCT GCC GCT ACT GCG GAC	65 409
L D L S H N A L Q R R P G W L A P L F CTC GAC CTG AGC CAC AAC GCG CTC CAG CGC CTG CGC CCC GGC TGG TTG GCG CCC CTC TTC	85 469
Q L R A L H L D H N E L D A L G R G V F CAG CTG CGC GCC CTG CAC CTA GAC CAC AAC GAA CTA GAT GCG CTG GGT CGC GGC GTC TTC	105 529
V N A S G L R L L D L S S N T L R A L G GTC AAC GCC AGC GGC CTG AGG CTG GAT CTA TCA TCT AAC ACG TTG CGG GCG CTT GGC	125 589

Fig. 19A

R	H	D	L	D	G	L	G	A	L	E	K	L	L	L	L	F	N	N	R	L	145
CGC	CAC	GAC	CTC	GAC	GGG	CTG	GGG	GCG	CTG	GAG	AAG	CTG	CTT	CTG	TTT	AAT	AAC	CGC	TTG	649	
V	H	L	D	E	H	A	F	H	G	L	R	A	L	S	H	L	Y	L	G	165	
GTG	CAC	TTG	GAC	GAG	CAT	GCC	TTC	CAC	GGC	CTG	CGC	GCG	CTC	AGC	CAT	CTC	TAC	CTG	GGC	709	
C	N	E	L	A	S	F	S	F	D	H	L	H	G	L	S	A	T	H	L	185	
TGC	AAC	GAA	CTC	GCC	TCG	TTC	TCC	TTC	GAC	CAC	CTG	CAC	GGT	CTG	AGC	GCC	ACC	CAC	CTG	769	
L	T	L	D	L	S	S	N	R	L	G	H	I	S	V	P	E	L	A	A	205	
CTT	ACT	CTG	GAC	CTC	TCC	TCC	AAC	GCG	CTG	GGA	CAC	ATC	TCC	GTA	CCT	GAG	CTG	GCC	GCG	829	
L	P	A	F	L	K	N	G	L	Y	L	H	N	N	P	L	P	C	D	C	225	
CTG	CCG	GCC	TTC	CTC	AAG	AAC	GGC	CTC	TAC	TTG	CAC	AAC	AAC	CCT	TTG	CCT	TGC	GAC	TGC	889	
R	L	Y	H	L	L	Q	R	W	H	Q	R	G	L	S	A	V	R	D	F	245	
CGC	CTC	TAC	CAC	CTG	CTA	CAG	CAG	TGG	CAC	CAG	CGG	GGC	CTG	AGC	GCC	GTG	CGC	GAC	TTT	949	
A	R	E	Y	V	C	L	A	F	K	V	P	A	S	R	V	R	F	F	Q	265	
GCG	CGC	GAG	TAC	GTA	TGC	TTG	GCC	TTC	AAG	GTA	CCC	GCG	TCC	CGC	GTG	CGC	TTC	TTC	CAG	1009	
H	S	R	V	F	E	N	C	S	S	A	P	A	L	G	L	K	R	P	E	285	
CAC	AGC	CGC	GTC	TTT	GAG	AAC	TGC	TCG	TCG	GCC	CCA	GCT	CTT	GGC	CTA	AAG	CGG	CCG	GAA	1069	

**Fig. 19B**

E	H	L	Y	A	L	V	G	R	S	L	R	L	Y	C	N	T	S	V	P	305
GAG	CAC	CTG	TAC	GCG	CTG	GTG	GGT	CGG	TCC	CTG	AGG	CTT	TAC	TGC	AAC	ACC	AGC	GTC	CCG	1129
A	M	R	I	A	W	V	S	P	Q	Q	E	L	L	R	A	P	G	S	R	325
GCC	ATG	CGC	ATT	GCC	TGG	GTT	TCG	CCG	CAG	CAG	GAG	CTT	CTC	AGG	GCG	CCA	GGA	TCC	CGC	1189
D	G	S	I	A	V	L	A	D	G	S	L	A	I	G	N	V	Q	E	Q	345
GAT	GGC	AGC	ATC	GCG	GTG	CTG	GCC	GAC	GGC	AGC	TTG	GCC	ATA	GGC	AAC	GTA	CAG	GAG	CAG	1249
H	A	G	L	F	V	C	L	A	T	G	P	R	L	H	H	N	Q	T	H	365
CAT	GCG	GGA	CTC	TTC	GTG	TGC	CTG	GCC	ACT	GGG	CCC	CGC	CTG	CAC	CAC	AAC	CAG	ACG	CAC	1309
E	Y	N	V	S	V	H	F	P	R	P	E	P	E	A	F	N	T	G	F	385
GAG	TAC	AAC	GTG	AGC	GTG	CAC	TTT	CCG	CGC	CCA	GAG	CCC	GAG	GCT	TTC	AAC	ACA	GGC	TTC	1369
T	T	L	L	G	C	A	V	G	L	V	L	V	L	L	Y	L	F	A	P	405
ACC	ACA	CTG	CTG	GGC	TGT	GCC	GTG	GGC	CTT	GTG	CTC	GTG	CTG	CTC	TAC	CTG	TTC	GCC	CCA	1429
P	C	R	C	C	R	R	A	C	P	L	P	P	L	A	P	N	T	Q	P	425
CCC	TGC	CGC	TGC	TGC	CGT	GCC	TGC	TGC	CCG	CTG	CCG	CCG	CTG	GCC	CCA	AAC	ACC	CAG	CCC	1489
A	P	R	A	E	P	H	K	S	S	V	L	S	T	T	P	P	D	A	P	445
GCT	CCA	AGA	GCT	GAG	CCG	CAC	AAG	TCC	TCA	GTA	CTC	AGC	ACC	ACA	CCG	CCA	GAC	GCA	CCC	1549

**Fig. 19C**

S	P	Q	G	Q	A	S	T	S	T	*		
AGC	CCG	CAA	GGC	CAA	GCG	TCC	ACA	AGC	ACG	TAG	456	
											1582	
TCT	TTCT	GGAGCC	AGGCCG	GAGGGCC	CTCA	ATGGCC	CCGCGT	GCAGCT	GGCAGT	AGCTGAGGAATTCGATCTCTACAACC	1661	
CTG	AGGCC	CTGC	AGCTGA	AGGCTGG	CTCTG	AGTCCG	CCAGCTCC	ATAGGCTCCG	AGGGTCCC	CATGACAACTAGACTGC	1740	
CAG	GGCT	CCCCC	ACCC	AGCCCC	ACCC	CTCTTG	CTGCTCG	CCCTGCT	CCCTGCT	CCAGAGAACTGGCAGATACT	1819	
GGT	GGGA	GCAC	TGTGCC	CTGG	CCCCC	AGCTTC	CTGTAT	GGCCCTCG	AAACAAATGG	CCCTTCTCGCTCACTGGTAGA	1898	
GAC	AGGG	TTGT	GTCCCC	AACTGC	CTTCTG	CTCTG	CCCCCTG	CACAGAC	CCCAAAGG	CCCCCAGGCCCTGCAAGGTGTG	1977	
CTA	GTTC	CTGCT	TTCCCG	CGGACTT	CCCTAG	TGCCCC	AAATGCC	CTGTG	AGGCTG	AGACCCAGGCCCTGTGGCTTTCA	2056	
ACAC	AGCAC	AGCTGT	GGAA	AGTGG	CTGT	CTTCTAC	AGCC	TGTG	GAAGAAC	CCCTGTAGCAGAGCCTCCCATCCACCC	2135	
TC	AGGG	GCTG	AGGC	AGTGG	TGCTCA	AGAGCTG	ACGC	AGGG	CCACCT	CCCCCTCCCAAGGGGTGGAG	2214	
GG	AGTGG	GGCC	CAC	AGGAAA	AAGAG	GGGCTCTG	AAAGGA	AGATCT	CGCCC	CACACCC	CCAGGACAGAAAGGAAACAAGC	2293
CCG	CCCT	CTGG	TGAAA	ATGGG	ACTCCC	CTCCAT	CCACCA	ACACCC	AACTCCT	TGAAAAGCTTCACAACTTCACGCAGAGTCC	2372	
GGT	GGC	AGCAC	CCAGG	CAGGAA	AGGCTC	CTCA	AGAGG	TTCC	TGGT	CTGTGGCC	TAAGCCCCCAGCCAGAGGCCCTGCTC	2451

Fig. 19D

TCTCTGGCCCTGGGGCATCCACCGTTGTTCTGAAGGCAGAGCCCAATTCTGTGGGCTCACAAAGACACAGTGAAGGGGATC 2530  
ATGGCCCTGCACCCCTGCTTTTCAGCAGTAAAAAGCCCGAAAAAGCCTGGCGAGCATGGCCGAGCTGGGAGGGCCGAGCCG 2609  
GAACTCCACGTCCTCGAGAGCAGGAGCCTCTTAAAGGGCTGGCACTGGTCTCAGCCCTAATGGCTGAGGCGGTACCCCTGG 2688  
CTTCATATGCATCTCACTGCTCCCACCTGCAGGGGGGCAGGGAAGGGGGGTCTGGGAGCCCTTCATGTGTGGGGGCCGAG 2767  
CTGGGGGCCCCCATGGCCATCCTGGACCTCGCTGCTCCAGAGTTTAATAAAGGTAGCACATGCTTATTGCTAGAAAAAA 2846  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2895

**Fig. 19E**

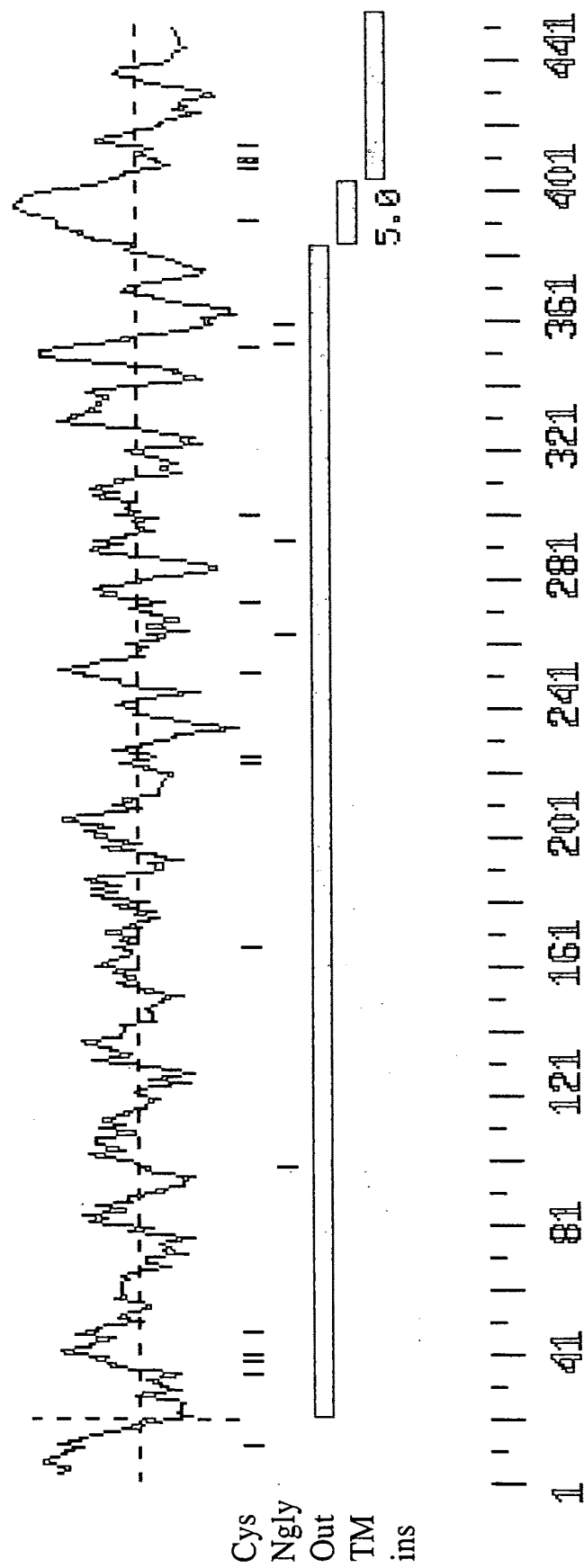


Fig. 19F

	10	20	30	40	50	60	70
H	MTWLVLLG	TLLCMLRV	GLGTPDSE	GFPFPRAL	HNCYPKCI	CAADLLSCT	GLGLQDVPAELPAATADL
	:	:	:	:	:	:	:
P	MN-LDIHCE	QLSDARWT	ELLPLLQ	QYEVRLDD	CGLTEEHCK	DIGS--AL	RANPSLT
	10	20	30	40	50	60	
	80	90	100	110	120	130	
H	NALQRLRP	GWLAFLF	QLRALHLD	HNELDAL	GRGVFVNA	---SGLRL	LLDSSNTLRALGRHDL-DGLGA-
	:	:	:	:	:	:	:
P	AGVHLVLQ	GLQSP	TKIQKLSL	QNC	SLTEAG	CGVLPST	LRSLPTLRELHLS
	70	80	90	100	110	120	130
	140	150	160	170	180	190	200
H	---LEKLL	LFNNRLV	HLD-EHAF	HGLRAL	SHLYLGC	NELASF	SFDHLHGLSATHLLTL
	:	:	:	:	:	:	:
P	QCHLEKLQ	LEYCRLT	AASCEPL	ASVLRAT	RAL----K	ELTVSNND	--IGEAGARVLGQGLAD-----SA
	140	150	160	170	180	190	
	210	220	230	240	250	260	
H	PELAALPA	FLKN-GL	YLHNNPL	PCDCRLY	HLLQRW	HQGLSA	VRDFAREYVCLAFKVPASVR---
	:	:	:	:	:	:	:
P	CQLETLR--	LENCGLT	PANCKD	LCGIVAS	QASLRELD	LGSNGLG	DAGIAELCPGLLSPASRLKTLWLWEC
	200	210	220	230	240	250	260

**Fig. 19G**



```

270      280      290      300      310      320
H SRVFENCSSA-PALGLKRPEEHLYALVGRSL-----RLYCNTSV-PAMRIAWVSPQQELLRAPGSRDGS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : :
P DITASGCRDLCRVLQAKETLKEL-SLAGNKLGDGARGLLCESLLQPGCQLES LWKSCSLTAACQHVSL
270      280      290      300      310      320      330

330      340      350      360      370      380      390
H AVLADGSLAIGNVQEQHAGLFVCLATGPRLLHHNQTHEYNVSVHFPRPEPEAFNTGFTLLGCAVGLVLVL
. . . . . : : : : : : : : : : : : : : : : : : : : : : : :
P MLTQNKHL-----LELQLSSNKLGDSGIQELCQALSQPGTTLRVLCLGDC EVTNSGCSSLAS--LLLANRS
340      350      360      370      380      390

400      410      420      430      440      450
H LYLFA PPCRRACPLPPLAPNTQPAPRAEPHK-SSVLSTTPPDAPSPQGQASTS-----T
: . . . . : : : : : : : : : : : : : : : : : : : : : : : :
P LRELDLSNNCVGDPGVLLQLLSLEQPGGCALEQLVLDYDTYWTTEEVEDRLQALEGSKPGLRVIS
400      410      420      430      440      450

```

**Fig. 19H**

ccg ttt ctc ttt aac cac ttg cac ggt ctg ggg tta acc cgc ctg cgg	48
Pro Phe Leu Phe Asn His Leu His Leu Gly Leu Thr Arg Leu Arg	
1 5 10 15	
act ctg gac ctc tcc tcc aac tgg ctg aaa cat atc tcc atc cct gag	96
Thr Leu Asp Leu Ser Ser Ser Asn Trp Leu Lys His Ile Ser Ile Pro Glu	
20 25 30	
ttg gct gca ctg cca act tat ctc aag aac agg agg ctc tac ctg cac aac	144
Leu Ala Ala Leu Pro Thr Tyr Leu Leu Lys Asn Arg Leu Tyr Leu His Asn	
35 40 45	
aac ccg ctg ccc tgt gac tgc agc ctc tac cac ctg ctc cgg cgc tgg	192
Asn Pro Leu Pro Cys Asp Cys Ser Leu Tyr His Leu Leu Arg Arg Trp	
50 55 60	
cac cag cgg ggc ctg agt gcc ctg cat gat ttt gaa cgc gag tac aca	240
His Gln Arg Gly Leu Ser Ala Leu His His Asp Phe Glu Arg Glu Tyr Thr	
65 70 75 80	
tgc ttg gtc ttt aag gtg tca gag tcc cga gtg cgc ttt ttt gag cac	288
Cys Leu Val Phe Lys Val Ser Glu Ser Glu Ser Arg Val Arg Phe Phe Glu His	
85 90 95	
agc cgg gtc ttc aag aac tgc tct gtg gct gca gct cca ggc tta gag	336
Ser Arg Val Phe Lys Asn Cys Ser Val Ala Ala Ala Pro Gly Leu Glu	
100 105 110	

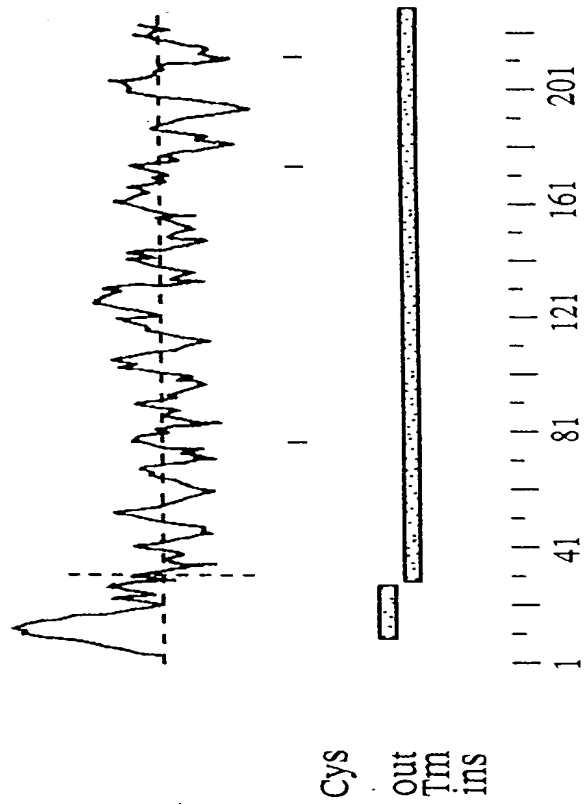
**Fig. 19I**

ctg cct gaa gag gag cag ctg cac gcg cag gtg ggc cag tcc ctg agg ctc	384
Leu Pro 115 Glu Glu Gln Gln Leu His 120 Ala Gln Val Gly Gln Ser 125 Leu Arg Leu	
ttc tgc aac acc agt gtg cct gcc act cgg gtg gcc tgg gtc tcc ccg	432
Phe Cys Asn Thr Ser Val Pro 135 Ala Thr Arg Val Ala 140 Trp Val Ser Pro	
aag aat gag ctg ctt gtg gcg cca gcc tct cag gat ggt agc atc gct	480
Lys Asn Glu Leu 150 Val Ala Pro Ala Ser Gln Asp Gly Ser 155 Ile Ala 160	
gtg ttg gct gat ggc agc tta gcc ata ggc agg gtg caa gag cag cac	528
Val Leu Ala Asp 165 Gly Ser Leu Ala Ile Gly Arg Val Gln Glu Gln His 175	
gca ggc gtc ttt gtg tgc ctg gcc agt ggg ccc cgc ctg cac cac aac	576
Ala Gly Val Phe 180 Val Cys Leu Ala Ser 185 Gly Pro Arg Leu 190 His His Asn	
cag aca ctt gag tac aat gtg agt gtg caa aag gct cgc ccc gag cca	624
Gln Thr Leu Glu Tyr Asn Val Ser 200 Val Gln Lys Ala Arg Pro Glu Pro 205	
gag act ttc aac aca ggc ttt acc acc ctg ctg ggc tgt att gtg ggc	672
Glu Thr Phe Asn Thr Gly Phe Thr Thr Leu Leu Gly Cys Ile Val Gly 210 215 220	

**Fig. 19J**

ctg gtg ctg gtg ttg ctg tac ttg ttt gca cca ccc tgt cgt ggc tgc	720
Leu Val Leu Val Leu Leu Tyr Leu Phe Ala Pro Pro Cys Arg Gly Cys	
225 230 235 240	
tgt cac tgc tgt cag cgg gcc tgc cgc aac cgt tgc tgg ccc cgg gca	768
Cys His Cys Cys Gln Arg Ala Cys Arg Asn Arg Cys Trp Pro Arg Ala	
245 250 255	
tcc agt cca ctc cag gag ctg agc gca cag tcc tcc atg ctt agc act	816
Ser Ser Pro Leu Gln Glu Leu Ser Ala Gln Ser Ser Met Leu Ser Thr	
260 265 270	
acg cca cca gat gca ccc agc cgc aag gcc agt gtc cac aag cat gtg	864
Thr Pro Pro Asp Ala Pro Ser Arg Lys Ala Ser Val His Lys His Val	
275 280 285	
gtc ttc ctg gag ccg ggc aag aag ggc ctc aat aat ggc cgt gtg cag ctc	912
Val Phe Leu Glu Pro Gly Lys Lys Gly Leu Asn Asn Gly Arg Val Gln Leu	
290 295 300	
gca gta cct cca gac tcc gat ctg tgc aac ccc atg ggc ttg caa ctc	960
Ala Val Pro Pro Asp Ser Asp Leu Cys Asn Pro Met Gly Leu Gln Leu	
305 310 315 320	
aa	962

**Fig. 19K**



**Fig. 19L**

```

M      1  ..... PFLFNHLHGLTRLRLTLDLSSNWLKHISI 30
H     151  HAFHGLRALSHLYLGCNELASFDFDHLHGLSATHLLTLDLSSNRLGHISV 200

M      31  PELAAALPTYLKNRLYLHNPNLPCDCSLYHLLRRWHQGLSALHDFEREYT 80
H     201  PELAAALPAFLKNGLYLHNPNLPCDCRLYHLLQRWHQGLSAVRDFAREYV 250

M      81  CLVFKVSESRVRFEEHSRVFKNCVAAAPGLELPEEQHQAQVGQSLRLFC 130
H     251  CLAFKVPASRVRFQHSRVFENCSSAPALGLKRPEEHLYALVGRSLRLYC 300

M     131  NTSVPATRVAVWSPKNELLVAPASQDGSIAVLADGSLAIGRVQEQHAGVF 180
H     301  NTSVPAMRIA WSPQQELLRAPGSRDGSIAVLADGSLAIGNVQEQHAGLF 350

M     181  VCLASGPRLHNNQTLEYNVSVQKARPEPEFTFNTGFTTLLGCIVGLVLL 230
H     351  VCLATGPRLHNNQTHEYNVSVHFPRPEPEAFNTGFTTLLGCAVGLVLL 400

M     231  YLFAPPCRGCHCCQACRNRCWPRASSPLQELSA.QSSMLSTTPPDAPS 279
H     401  YLFAPPCR...CCRRACPLPPLAPNTQAPAPRAEPHKSSVLSTTPPDAPS 446

M     280  RKASVHKHVVFLEPGKKGLNGRVQLAVPPDSDL CNP MGLQL 320
H     447  PQGQASTST..... 455

```

**Fig. 19M**

GTCGACCCACGCGTCCGGGAACCCAGCGTCCGCCGAC	M	A	W	T	K	Y	Q	L	F	L	10
	ATG	GCC	TGG	ACC	AAG	TAC	CAG	CTG	TTC	CTG	69
A G L M L V T G S I N T L S A K W A D N											30
GCC GGG CTC ATG CTT GTT ACC GGC TCC ATC AAC ACG CTC TCG GCA AAA TGG GCG GAC AAT											129
F M A E G C G G S K E H S F Q H P F L Q											50
TTC ATG GCC GAG GGC TGT GGA GGG AGC AAG GAG CAC AGC TTC CAG CAT CCC TTC CTC CAG											189
A V G M F L G G E F S C L A A A F Y L L R C											70
GCA GTG GGC ATG TTC CTG GGA GAA TTC TCC TGC CTG GCT GCC TTC TAC CTC CTC CGA TGC											249
R A A G Q S D S S V D P Q Q Q P F N P L L											90
AGA GCT GCA GGG CAA TCA GAC TCC AGC GTA GAC CCC CAG CAG CCC TTC AAC CCT CTT CTT											309
F L P P A A L C D M T G T S L M Y V A L N											110
TTC CTG CCC CCA GCG CTC TGT GAC ATG ACA GGG ACC AGC CTC ATG TAT GTG GCT CTG AAC											369
M T S A S S F Q M L R G A V I I F T G L											130
ATG ACC AGT GCC TCC AGC TTC CAG ATG CTG CGG GGT GCA GTG ATC ATA TTC ACT GGC CTG											429
F S V A F L G R R R L V L S Q W L G I L A											150
TTC TCG GTG GCC TTC CTG GGC CGG AGG CTG GTG CTG AGC CAG TGG CTG GGC ATC CTA GCC											489

**Fig. 20A**

T	I	A	G	L	V	V	V	G	L	A	D	L	L	S	K	H	D	S	Q	170
ACC	ATC	GCG	GGG	CTG	GTG	GTC	GTG	GGC	CTG	GCT	GAC	CTC	CTG	AGC	AAG	CAC	GAC	AGT	CAG	549
H	K	L	S	E	V	I	T	G	D	L	L	I	I	M	A	Q	I	I	V	190
CAC	AAG	CTC	AGC	GAA	GTG	ATC	ACA	GGG	GAC	CTG	TTG	ATC	ATC	ATG	GCC	CAG	ATC	ATC	GTT	609
A	I	Q	M	V	L	E	E	K	F	V	Y	K	H	N	V	H	P	L	R	210
GCC	ATC	CAG	ATG	GTG	CTA	GAG	GAG	AAG	TTC	GTC	TAC	AAA	CAC	AAT	GTG	CAC	CCA	CTG	CGG	669
A	V	G	T	E	G	L	F	G	F	V	I	L	S	L	L	L	V	P	M	230
GCA	GTT	GGC	ACT	GAG	GGC	CTC	TTT	GGC	TTT	GTG	ATC	CTC	TCC	CTG	CTG	CTG	GTG	CCC	ATG	729
Y	Y	I	P	A	G	S	F	S	G	N	P	R	G	T	L	E	D	A	L	250
TAC	TAC	ATC	CCC	GCC	GGC	TCC	TTC	AGC	GGA	AAC	CCT	CGT	GGG	ACA	CTG	GAG	GAT	GCA	TTG	789
D	A	F	C	Q	V	G	Q	Q	P	L	I	A	V	A	L	L	G	N	I	270
GAC	GCC	TTC	TGC	CAG	GTG	GGC	CAG	CAG	CCG	CTC	ATT	GCC	GTG	GCA	CTG	CTG	GGC	AAC	ATC	849
S	S	I	A	F	F	N	F	A	G	I	S	V	T	K	E	L	S	A	T	290
AGC	AGC	ATT	GCC	TTC	TTC	AAC	TTC	GCA	GGC	ATC	AGC	GTC	ACC	AAG	GAA	CTG	AGC	GCC	ACC	909
T	R	M	V	L	D	S	L	R	T	V	V	I	W	A	L	S	L	A	L	310
ACC	CGC	ATG	GTG	TTG	GAC	AGC	TTG	CGC	ACC	GTT	GTC	ATC	TGG	GCA	CTG	AGC	CTG	GCA	CTG	969

**Fig. 20B**



G	W	E	A	F	H	A	L	A	L	Q	I	L	G	F	L	I	L	L	I	G	T	330	
GGC	TGG	GAG	GCC	TTC	CAT	GCA	CTG	CAG	ATC	CTT	GGC	TTC	CTC	ATA	CTC	CTT	ATA	GGC	ACT	1029			
A	L	Y	N	G	L	H	R	P	L	L	G	R	L	S	R	G	R	P	L	350			
GCC	CTC	TAC	AAT	GGG	CTA	CAC	CGT	CCG	CTG	CTG	GGC	CGC	CTG	TCC	AGG	GGC	CGG	CCC	CTG	1089			
A	E	E	S	E	Q	E	R	L	L	G	G	T	R	T	P	I	N	D	A	370			
GCA	GAG	GAG	AGC	GAG	CAG	GAG	AGA	CTG	CTG	GGT	GGC	ACC	CGC	ACT	CCC	ATC	AAT	GAT	GCC	1149			
S	*																			372			
AGC	TGA																			1155			
GGT	TCC	CTG	GAG	GGC	TCT	ACT	GCC	ACCC	GGG	TGCT	CTC	CTT	CTC	CTG	AGACT	GAG	GCC	CAC	ACAGG	CTGGT	GGG	CCCCGAA	1234
TGCC	CTAT	CCCCA	AGGC	CTCAC	CCCT	GTCC	CCCT	CTCC	CTGC	AGAAC	CCCCC	AGGG	CAGCT	GTGCC	ACAG	AAGATA	ACAAC	AC	1313				
CCA	AGT	CCCT	CTTT	CTCA	CTAC	CACT	ACCA	CCCT	GCAG	GGT	GGT	GTAT	ACCC	AGCCCC	CAAG	CCCT	GAGT	GCAGT	GGC	AGAC	CTC	1392	
AGC	CTCT	GGAC	CCCT	CTAC	AGCA	CTAG	AGCT	AAAT	CAT	GAAG	TTGA	ATTG	TAGG	AAATT	TACCA	CCCGT	AGT	GTAT	CTG	1471			
AAT	CATA	AACT	AGAT	TAT	CATA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	1518			

Fig. 20C

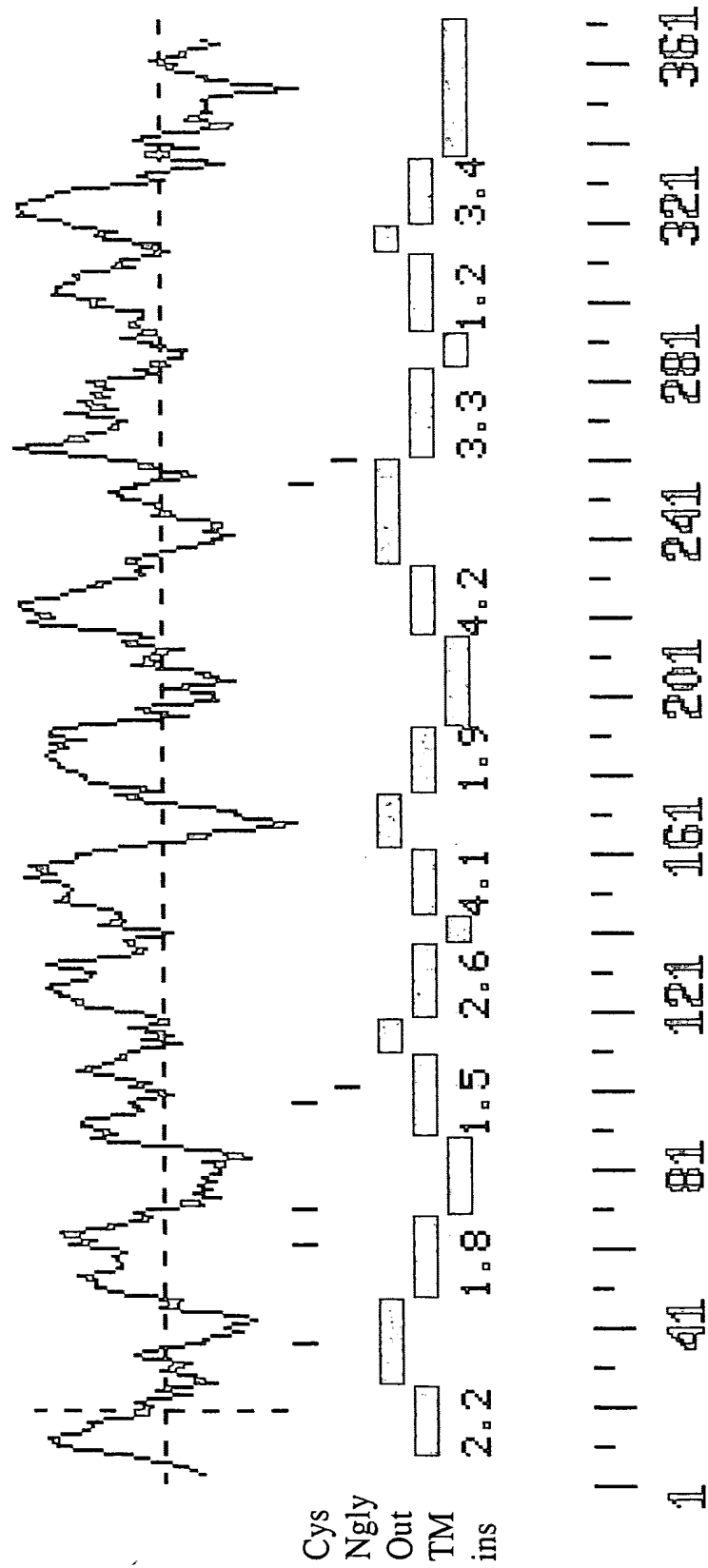


Fig. 20D

	M	A	P	H	W	
GTCGACCCACGCGTCCGGGACAGCTGGCCTGAAGCTCAGAGCCGGGCGTGCGCC	ATG	GCC	CCA	CAC	TGG	5
						72
A V W L L A A R L W G L G I G A E V W W						25
GCT GTC TGG CTG CTG GCA AGG CTG TGG GGC CTG GGC ATT GGG GCT GAG GTG TGG TGG						132
N L V P R K T V S S G E L A T V V R R F						45
AAC CTT GTG CCG CGT AAG ACA GTG TCT TCT GGG GAG CTG GCC ACG GTA GTA CGG CGG TTC						192
S Q T G I Q D F L T L T L T E P T G L L						65
TCC CAG ACC GGC ATC CAG GAC TTC CTG ACA CTG ACG CTG ACG GAG CCC ACT GGG CTT CTG						252
Y V G A R E A L F A F S M E A L E L Q G						85
TAC GTG GGC GCC CGA GAG GCC CTG TTT GCC TTC ATG GAG GCC CTG GAG CTG CAA GGA						312
A I S W E A P V E K K T E C I Q K G K N						105
GCG ATC TCC TGG GAG GCC CCC GTG GAG AAG AAG ACT GAG TGT ATC CAG AAA GGG AAG AAC						372
N Q T E C F N F I R F L Q P Y N A S H L						125
AAC CAG ACC GAG TGC TTC AAC TTC ATC CGC TTC CTG CAG CCC TAC AAT GCC TCC CAC CTG						432
Y V C G T Y A F Q P K C T Y V V S A A L						145
TAC GTC TGT GGC ACC TAC GCC TTC CAG CCC AAG TGC ACC TAC GTC GTG AGT GCT GCC CTC						492

**Fig. 21A**

L	P	R	C	P	P	Q	P	P	A	L	L	T	L	L	W	T	R	G	C	G	165
CTA	CCT	CGG	TGT	CCC	CAG	CCC	CCC	CCC	GCC	CTC	CTC	ACC	CTT	CTC	TGG	ACT	CGT	GGA	TGT	GGC	552
P	Q	S	P	A	L	K	H	L	L	L	I	T	S	L	S	V	L	R	T	C	185
CCA	CAG	AGC	CCT	GCC	CTT	AAG	CAT	CTC	CTC	ATC	ACC	TCT	CTC	TCT	GTC	CTT	AGA	ACA	TGC	612	
S	P	S	L	W	S	M	E	S	L	K	M	G	R	A	S	V	P	M	T	205	
TCA	CCT	TCA	CTT	TGG	AGC	ATG	GAG	AGT	TTG	AAG	ATG	GGA	AGG	GCA	AGT	GTC	CCT	ATG	ACC	672	
Q	L	R	A	M	L	A	F	L	W	M	V	S	C	T	R	P	H	S	T	225	
CAG	CTA	AGG	GCC	ATG	CTG	GCC	TTC	TTG	TGG	ATG	GTG	AGC	TGT	ACT	CGG	CCA	CAC	TCA	ACA	732	
T	S	W	A	R	N	P	L	S	C	V	T	W	G	P	T	T	P	*		244	
ACT	TCC	TGG	GCA	CGG	AAC	CCA	TTA	TCC	TGC	GTA	ACA	TGG	GGC	CCC	ACC	ACT	CCA	TGA		789	
AGACAGAGTACCTGGCCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTGCCCTATGTACCTGAGAGTGTGGCAGCTT																				868	
CACGGGGACGACGACAAGGTCTACTTCTTCTTCAGGGAGCGGGCAGTGGAGTCCGACTGCTATGCCGAGCAGGTGGTG																				947	
GCTCGTGTGGCCCGTGTCTGCAAGGGCGATATGGGGGGCGCACGGACCCCTGCAGAGGAAGTGGACCACGTTCCCTGAAGG																				1026	
CGCGGCTGGCATGCTCTGCCCCGAACTGGCAGCTCTACTTCAACCAGCTGCAGGGCGATGCACACCCCTGCAGGACACCTC																				1105	

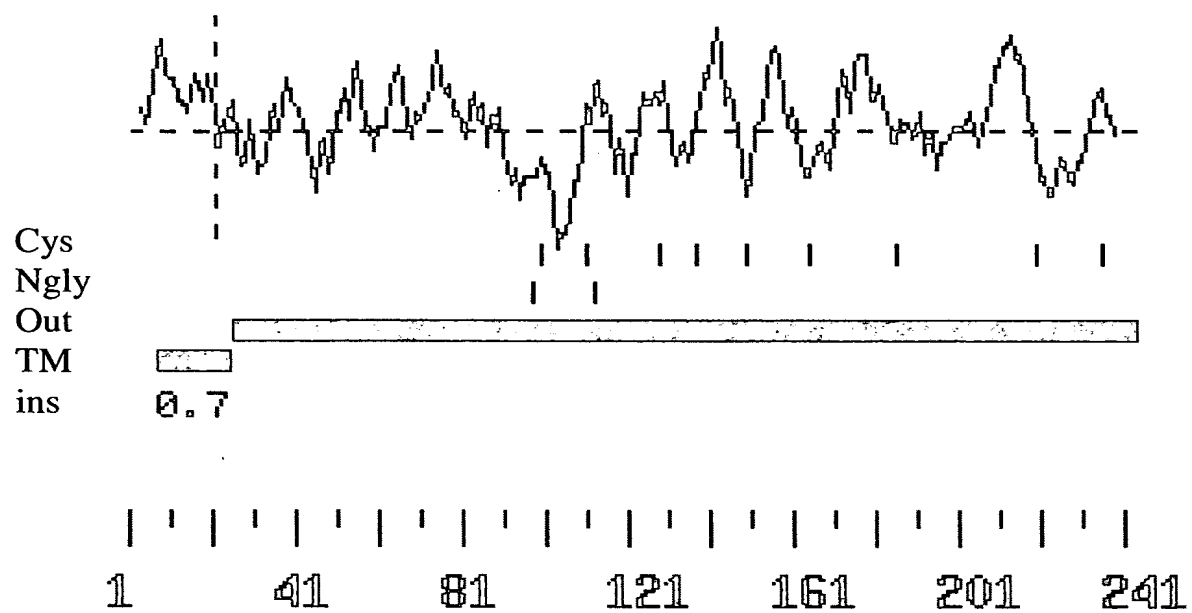
**Fig. 21B**

CTGGCACAACACCTTCTTTGGGGTTTTCAGCACAGTGGGTGACATGTACCTGTGCGCCATCTGTGAGTACCAG 1184  
TTGGAAGAGATCCAGCGGTGTTTGAGGGCCCCCTATAAGGAGTACCATGAGGAAGCCCCAGAAAGTGGGACCGCTACACTG 1263  
ACCCTGTACCCAGGCCCTGGTTGTGATGGCTGCCCCAGCCCCGCAATGCCGGGCTACCACTGCTTTTCAGAGGAGCAG 1342  
GGGGCGGGCTGGCTGCTGAAGCTACCTTGTGGCTGTCGTGGCAGGCCCTCGGTGACCTTGGAGGCCCGGGCCCCC 1421  
TGGAAAACTGGGGCTGGTGTGGCTGGCGGTGGTGGCCCCCTGGGGGCTGTGTGCCCTGGTGTGCTGCTGGTGTCTGTC 1500  
ATTGCGCCGGCGCTGCGGGAAGAGCTGGAGAAAGGGCCAAAGGCTACTGAGAGGACCTTGGTGTACCCCCCTGGAGCTG 1579  
CCCAAGGAGCCCAACAGTCCCCCTTCCGGCCCCCTGTCCTGAAACCAGATGAGAAACTTTGGGATCCTGTGCGTTACTACT 1658  
ATTCAGATGGCTCCCTTAAGATAGTACCTGGGCATGCCCGGTGCCAGCCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGG 1737  
CATCCCAGGCCAGCCTCTGCCCTTCTCCAACCTCGGCTTCACCTGGGGGGTGGGCGGAACTCAAATGCCAAATGGTTACGTG 1816  
CGCTTACAAC TAGGAGGGAGGACCGGGGAGGGCTCGGGCACCCCCCTGCCCTGAGCTCGCGGATGAAC TGAGACGCAAAC 1895  
TGCAGCAACGCCAGCCACTGCCCCGACTCCAACCCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCCGCTCGGCGGGA 1974  
AGCGTGGAGGTAGCTCCTACTTTTGACACAGGCACCAAGCTACCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGG 2053

**Fig. 21C**

GACAGATACTGCCCAGCACCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACCTGCCACTTGGTGTGGCTCAC 2132  
CAGGGCACCCAGCCTCGCAGAAAGGCATCTTCCCTCCTCTCTGTGAATCACAGACACGCGGGACCCAGCCGCCAAAACTTT 2211  
TCAAGGCAGAAAGTTTCAAGATGTGTGTTTGTCTGTATTTGCACATGTGTTTGTGTGTGTATGTGTGTGCACGC 2290  
GCGTGCGCGCTTGTGGCATAGCCCTTCCGTGTTTCTGTCAAAGTCTTCCCTTGGCCCTGGGTCCCTCGGTGAGTCATTGGAG 2369  
CTATGAAGGGAAAGGGTCCGTATCACTTTTGTCTCTCTACCCCCACTGCCCCGAGTGTGCGGCAGCGATGTACATATGG 2448  
AGGTGGGTGGACAGGGTGTGTGCCCCCTTCAGAGGGAGTGCAGGGCTTGGGGTGGGCCCTAGTCCCTGCTCCCTAGGGCTG 2527  
TGAAATGTTTTCAGGGTGGGGGAGGAGATGGAGCCCTCCTGTGTGTTTGGGGGGAAGGTTGGGTGGGGCCCTCCCACCTG 2606  
GCCCCGGGTTCAGTGGTATTTTATACTTGCCCTTCTTCCCTGTACAGGGCTGGGAAAGGCTGTGTGAGGGGAGAGAAGGG 2685  
AGAGGGTGGCCCTGCTGTGGACAAATGGCATACTCTCTTCCAGCCCTAGGAGGGGCTCCTAACAGTGTAACCTTATTGT 2764  
GTCCCCGCGTATTATTGTTGTAATAATTTGAGATTTTATATTGA 2811

**Fig. 21D**



**Fig. 21E**





```

360      370      380      390      400      410      420
M QAQKWARYTDPVSPRPGSCINNWHRDNGYTSSLELPDNTLNFIKKHPLMEDQVKPRLGRPLLKKNTNF
  ::      ::      ::      ::      ::      ::      ::
H ---WTR-----GCGPQ-----SPAL-----KH-----LLI-----TSL
160                                     170

430      440      450      460      470      480      490
M THVVADRVPGLDGATYTVLFIGTGDGWLKAVSLGPWIHMVEELQVFDQEPVESLVLSQSKKVLFAGSRS
  .      .      .      .      .      .      .
H S-----VLRTCSPSLW-----SMESLKMGRA-----SVPMT
180                                     190      200

500      510      520      530      540      550      560
M QLVQLSLADCTKYRFCVDCVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYGIKKVR
  ::      ::      :      :      :      :      :
H QLRAM-LA-----F-----L-----WMVSCTRPHSTTS-----
210                                     220

570      580      590      600      610      620      630
M SIPKNITVSGTDLVLPCHLSSNLAAHAWTFGSQDLPAEQPGSFLYDTGLQALVVMAAQSRHSGPYRCYS
  :
H -----W-----

640      650      660      670      680      690      700
M EEQTRLAESYLVAVVAGSSVTLEARAPLENLGLVWLAVVALGAVCLVLLLVLVSLRRLREELEKGAK
  ::      ::      ::      ::      ::      ::      ::
H -----ARNPLS-----CVT-----
230

```

**Fig. 21G**

```

710      720      730      740      750      760      770
M ASERTLVYPLELPKEPASPPFRPGPETDEKLWDVPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQP
H -----W-----GPTTP-----
      :
      :: ::
      240

780      790      800      810      820      830
M LPSPTRLHLGGGRNSNANGYVRLQLGGEDRGSGHPLPELADELRRKLQQRQLPDSNPRESSV
H -----

```

**Fig. 21H**

```

10      20      30      40      50      60      70
M  GGCACGAGGTGGCCGGAGTCAAAACGCGAGGCGAGCCAGGGATTGGAGCTGCACGAAAGAGGGCTGCTG
:  :      :      :      :      :      :      :      :      :      :      :
H  GTC-----GACC-----CACG-----CGTC-----CGCG-----GGACAGCTG
10      20

80      90      100     110     120     130     140
M  GACTGAAGTTTAGACCCCTGGGTGCTGCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAGGGCT
:  :      :      :      :      :      :      :      :      :      :      :
H  GCCTGAAGCTCAGAGCCGGGGCTGCGCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAAGGCT
30     40     50     60     70     80     90

150     160     170     180     190     200     210
M  GTGGGGCCCTGGGCATCGGGGCTGAGATGTGGTGAACCTTGTGCCCGGGAAGACAGTATCTTCTGGGAG
:  :      :      :      :      :      :      :      :      :      :      :
H  GTGGGGCCCTGGGCATTTGGGGCTGAGGTGTGGTGAACCTTGTGCCCGGTAAGACAGTGTCTTCTGGGAG
100    110    120    130    140    150    160

220     230     240     250     260     270     280
M  CTGGTCACAGTAGTGAGGCGGTTCTCCCAGACAGGCATCCAGGACTTCCTGACACTGACCCCTGACAGAAC
:  :      :      :      :      :      :      :      :      :      :      :
H  CTGGCCACGGTAGTACGGCGGTTCTCCCAGACCGGCATCCAGGACTTCCTGACACTGACGCTGACGGAGC
170    180    190    200    210    220    230

290     300     310     320     330     340     350
M  ATTCTGGCCCTTTTATATGTGGGGGCCCCGAGAGGGCGCTGTTTGCCCTTCAGTGTAGAGGCTCTGGAGCTGCA
:  :      :      :      :      :      :      :      :      :      :      :
H  CCACTGGGCTTCTGTACGTGGGGCGCCCCGAGAGGCCCTGTTTGCCCTTCAGCATGGAGGCCCTGGAGCTGCA
240    250    260    270    280    290    300

```

**Fig. 21I**



```

710      720      730      740      750      760      770
M TCAAGACAGAGTACCTGGCTTTTGGCTGAATGAACCCACACTTTGTAGGCTCTGCCCTTTGTCCCTGAGAG
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----AGAGCCCTGCCCTTAAGC-----ATCTCCTCATCAC---CTCTCTCTCTGTCC-TTAGA-
560      570      580      590      600

780      790      800      810      820      830      840
M TGTGGGAAGCTTCACGGGAGACGATGACAAGATCTACTTCTTCTTCAGTGAGCGGCGAGTGGAGTATGAC
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----ACATGCTCACCTTCA-CTT-TG-GAGCA---TGGAGAGTTTGA-
610      620      630      640

850      860      870      880      890      900      910
M TGCTATTCGAGCAGGTGGTGGCTCGTGTGGCGAGAGTCTGTAAGGTGACATGGGGGAGCACGGACGC
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H -----AGATGG-----GAAGGGCAAGTGTC-----C-----CTATGACCC
650      660      670

920      930      940      950      960      970      980
M TGCAGAAATAATGGACGACGTTCCCTGAAGGCTCGGTTGGTGTGCTCAGCCCCCTGACTGGAAGGTCTACTT
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H AGCTAAGGGCCATGCTGGCCCTTCTTGT-GGATGGTGAGCTGTACTCGGCCAC--ACT-----CAACAA
680      690      700      710      720      730

990      1000     1010     1020     1030     1040     1050
M CAACCAGCTGAAGCGGTGCACACCCCTGCCGGGCGCCTCTTTGGCACAAACACCACCTTCTTCGGGGTTTTT
  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::  ::  :::::
H CTTCCCTG-----GGCA-----CGGAAC-CCA-TTATC-----CTGCG-----TAA
740      750      760

```

**Fig. 21K**

```

1060      1070      1080      1090      1100      1110      1120
M CAAGCGGATGGGGCGATATGGACCTGTCTGCAGTTTGTGAGTACCAGTTGGAACAGATCCAGCAAGTGT
::      :::::      ::      :      ::::      :      ::::
H CA-----TGGGGC-----CC--C-----ACCA-----C---TCCA-----
770
1130      1140      1150      1160      1170      1180      1190
M TTGAGGGTCCCTACAAGGAGTACAGTGAGCAAGCCAGAGTGGCCCCGTATACTGACCCGGTACCCAG
:::::      ::      :::::      :::::      :      :      :      :      :
H -TGAAG-----ACA--GAGTAC-----CTGGCC---TTTGGCTCAACGAACCTCACTTTGTA---GG
790      800      810      820      830
1200      1210      1220      1230      1240      1250      1260
M CCCTCGGCCTGGTTTCGTGTATCAACAACCTGGCACCGAGACAATGGCTACACCAGTTCCTGGAACGTCCG
:      ::      :::::      :      :      :      :      :      :      :
H C--TCTGCCTA-----TGTA-C-----CTGA----GAGT-GTGGGCAGCTTCA---CGGGGGACGAC--
840      850      860      870      880
1270      1280      1290      1300      1310      1320      1330
M GACAACACCCCTCAACTTCATCAAGAAGCACCCCTGATGGAGGACCAGGTGAAGCCTCGGTTGGGCCGCC
:::::      :      :::::      :::::      :      :      :      :      :
H GACAAGGTCTACTTCTTCTTCAGGGAGC-----GGGC--AGTGGAGTC-CGA-----
890      900      910      920
1340      1350      1360      1370      1380      1390      1400
M CCCTACTTGTGAAGAAGAACACTAACTTCACACACGTGGTGGCCGACAGGGTCCCAGGGCTTGATGGTGC
:::::      ::      :      ::      :::::      :      :      :      :
H --CTGCTA-----TGC--CGAGCAGGTGGTGGC-----TC-----GTGTGGC
930      940      950

```

Fig. 21L

```

1410      1420      1430      1440      1450      1460      1470
M CACCTATACAGTGTGTTTCATTGGTACAGGAGATGGCTGGCTGCTGAAGCTGTGAGCCCTGGGGCCCTGG
:  :  .  .  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H C--CGTGTCTG-----CAAGGG--C--GATATGGGGGC-----GCA-----C--GGACCCCTG-
960      970      980      990

1480      1490      1500      1510      1520      1530      1540
M ATCCACATGGTGGAGGAACTGCAGGTGTTTGACCAAGGAGCCAGTGGAAGTCTGGTGTCTCTCAGAGCA
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H -----GAGGAA-----GTG-----GACCACGTTCCCTG-----AAGGC-----GCGG---CTG-GCA
1000      1010      1020      1030

1550      1560      1570      1580      1590      1600      1610
M AGAAGGTGCTCTTTGCTGGCTCCCGCTCTCAGCTGGTTTCAGCTGTCTCTGCGCCGACTGCACAAAGTACCG
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H -----TGCTCT-----GC-CCCGAACT-GGCAG-CTCTACT-TCA---ACCAGCTGCA---GG---CG
1040      1050      1060      1070      1080

1620      1630      1640      1650      1660      1670      1680
M TTTCTGTAGACTGTGTCTCTGGCCAGGAGCCCTTACTGTGCCCTGGAATGTCAACACCAGCCGCTGTGTG
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H ATGC-----ACA---CCCTG--CAGGACACCT-----CCTGGCA---CAACACCACCTTCTTTTGGG
1090      1100      1110      1120      1130

1690      1700      1710      1720      1730      1740      1750
M GCCACCACCAAGTGGTCGCTCGGGGTCCTTTCTGGTCCAACATGTGGCGAACTTGGACACTTCAAAGATGT
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
H GTTT--TTCAA-----GCACAGTGG-----GGT--GACATGTACCTGTC---GGC-CATCTG---TGA
1140      1150      1160      1170

```

**Fig. 21M**

```

1760      1770      1780      1790      1800      1810      1820
M GTAACCAAGTATGGCATTAATAAAGTCAGATCTATTCCCAAGAACAATCACCGTTGTGTCAAGGCACAGACCT
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H GTA-CCAGT-TGG-----AAG--AGATC-----CAGCG--GGTGTTTGAGG-----
1180      1190      1200      1210

1830      1840      1850      1860      1870      1880      1890
M GGTCCTACCCCTGCCACCTCTCGTCCAATTGGCCCATGCCCACTGGACCTTCGGAAGCCAGGACCTGCCT
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H -----GCC-----CCTATAAGGA--GTACC--ATGA-----GGAAGC-----CCA
1220      1230      1240

1900      1910      1920      1930      1940      1950      1960
M GCAGAAACAACCTGGCTCCTTTCTTATGACACGGGACTCCAGGCGCTGGTGGTATGCCCCGACAGTCCC
   : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H GAAGTGGGACC--GCTAC--ACT---GACCCCTGTAC-CCAGGCCCTGGTGTGTGATGGCTGCCCAGCCCC
1250      1260      1270      1280      1290      1300

1970      1980      1990      2000      2010      2020      2030
M GTCACCTCTGGACCCCTATCGTTGCTATTTCAGAGGAGCAGGGGACAAGACTGGCTGCAGAAAGCTACCTTGT
   : :: : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H GCCATGCCGGGGCCTACCACTGCTTTTCAGAGGAGCAGGGGGCGCGGCTGGCTGCTGAAGGCTACCTTGT
1310      1320      1330      1340      1350      1360      1370

2040      2050      2060      2070      2080      2090      2100
M TGCTGTCTGGCCGGCTCGTCTGGTGACACTGGAGGCACGGGCTCCCTTGGAACCACTGGGGCTCGTGTGG
   : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H GGCTGTCTGGCAGGCCCGTCTGGTGACCTTGGAGGCCCGGGCCCCCTGGAAAAACCTGGGGCTGGTGTGG
1380      1390      1400      1410      1420      1430      1440

```

**Fig. 21N**



[illegible]

**Fig. 210**

```

2460      2470      2480      2490      2500      2510      2520
M CTCAAATGCCAATGGTTATGTGCGTTTACAGTTGGCGGAGAGAGACCAGAGGATCTGGGCACCCACTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CTCAAATGCCAATGGTTACGTGCGCTTACAACCTAGGAGGGAGGACCGGGAGGGCTCGGGCACCCCTG
1800      1810      1820      1830      1840      1850      1860

2530      2540      2550      2560      2570      2580      2590
M CCTGAGCTCGCGGATGAATTACGACGGAACTACAACAGCGCCAGCCGCTGCCCTGACTCCAACCCAGAGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CCTGAGCTCGCGGATGAACCTGAGACGCAAACTGCAGCAACGCCAGCCACTGCCCGACTCCAACCCCGAGG
1870      1880      1890      1900      1910      1920      1930

2600      2610      2620      2630      2640      2650
M AGTCCTCAGTATGAGGGACCCCCCACCCTCATTTGGCGGGGGGCTCTCATGGGAGGTGCA-CTCTTAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H AGTCATCAGTATGAGGGGAACCCCC-ACCGCGTCGCGGGAAG-----CGTGGAGGTGTAGCTCCTA-
1940      1950      1960      1970      1980      1990

2660      2670      2680      2690      2700      2710      2720
M CTTTGCACAGGCACCACTACCTCAGGGACATGGCAGGGGCACCTTGCTCTGCCCTGGGACAGACACTGCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CTTTGCACAGGCACCACTACCTCAGGGACATGGCAGGGGCACCTGCTCTGTCTGGGACAGATACTGCC
2000      2010      2020      2030      2040      2050      2060

2730      2740      2750      2760      2770      2780      2790
M CATCATTTGCCCCGGCGTGAGGACCTGCTC-----AGCATGGGCACCTGCCACTTGGTGTGGCTCACCAGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H CAGCACCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACCTGCCACTTGGTGTGGCTCACCAGG
2070      2080      2090      2100      2110      2120      2130

```

**Fig. 21P**

```

2800      2810      2820      2830      2840      2850      2860
M ACTTCAGCCTCACAGGAGACA-CACCCCTCCTCT--GTGAATTGAGACATGTGGGACCCAGCAGCCAAA
.. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GCACCAGCCTCGCAGAAGGCATCTTCCTCCTCTCTGTGAATCACAGACACGCGGACCCAGCCGCCAAA
2140      2150      2160      2170      2180      2190      2200

2870      2880      2890      2900      2910      2920
M ACTTTGCAAGGAAGAGGTTTCAAGATGTGGCGTGTTTGTGCAT--ATATGTGTTGGTATGCATGTGGAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ACTTTTCAAGGCAGAGTTTCAAGATGTGTGTTTGTCTGTATTTGCACATGTGTTTGTGTGTGTGTAT
2210      2220      2230      2240      2250      2260      2270

2930      2940      2950      2960      2970      2980      2990
M GAATGTGTGTGTGTGTGTG---TGTTGTGTAACTTTCCTGTCTCTATCACGTCTTCCCTTGGCCTGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTGTGTGTGCACGCGGTGCGCGCTTGTGGCATAGCCTTCCCTGTTCCTGTTCGTCAAGTCTTCCCTTGGCCTGG
2280      2290      2300      2310      2320      2330      2340

3000      3010      3020      3030      3040      3050      3060
M GGTCCTCCTGGTTGAGTCTTTGGAGCTATGAAGGGAAGGGGTCATAGCACTTTGCTTCTCCTACCCCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H G-TCCCTCCTGGT-GAGTCATTGGAGCTATGAAGGGAAGGGG-TCGTATCACTTTGTCTCTCCTACCCCC
2350      2360      2370      2380      2390      2400      2410

3070      3080      3090      3100      3110      3120      3130
M AGCTGTCCCAAGCTTTGGGGCAGTGATGTACATACGGGGAAGGAAGACAGGGTGTGTACCCCTTTTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H A-CTGCCCCGAG-TGTCGGGCACGATGTACATATGGAGGTGGGTGGACAGGGTGTGTGCCCCCTTCAG
2420      2430      2440      2450      2460      2470      2480

```

**Fig. 21Q**

```

3140      3150      3160      3170      3180      3190      3200
M GGGAGTGGGGACTCGGGGTGGGCCCTAGCCCTGCTCCTAGGGCTGTGAATGTTTTCAGGGCGGGGTT
.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H AGGAGTGCAGGGCT-TGGGGTGGGCCCTAGTCCCTGCTCCTAGGGCTGTGAATGTTTTCAGGGTGGGGGA
2490      2500      2510      2520      2530      2540      2550

3210      3220      3230      3240      3250      3260      3270
M GGGGTGGAGATGGAACCTCCTGC---TTCAGGGGAGGGGTGGGCAGGGCCTCCCACTTGCCCTCCGGG
::: .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H GGG-----AGATGGAGCCTCCTGTGTGTTTGGGGGAAGGGTGGGTGGGCCCTCCCACTTGCCCCCGGGG
2560      2570      2580      2590      2600      2610

3280      3290      3300      3310      3320      3330
M TTCGGTGGTATTTATATTTCGCTCTTC-TG-ACAGGCTGGGAAGG--TTGTTGGGGAGGAAGGG
:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H TTCAGTGGTATTTATACTTGCCTTCTTCCTGTACAGGCTGGGAAGGCTGTGTGAGGGGAGAGAAGGG
2620      2630      2640      2650      2660      2670      2680

3340      3350      3360      3370      3380      3390      3400
M AGGAGGTGGGCATGCTATGGATACTGGCCTATCCTCTCCCTGCTCTGGGAAAAGGCT---AACAGTGA
:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H AGAGGGTGGGCCCTGCTGTGGACAATGGCATACTCTCTTCCAGCCCTAGGAGGAGGCTCCTAACAGTGA
2690      2700      2710      2720      2730      2740      2750

3410      3420      3430      3440      3450      3460      3470
M ACTTATTGTGTCCCCACATATTTATTGTTGTAAATATTGAGTATTTTATATTGACAAAATAAATGGA
:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.
H ACTTATTGTGTCCCCCGTATTTATTGTTGTAAATATTGAG-ATTTTATATTGA-----
2760      2770      2780      2790      2800      2810

```

**Fig. 21R**

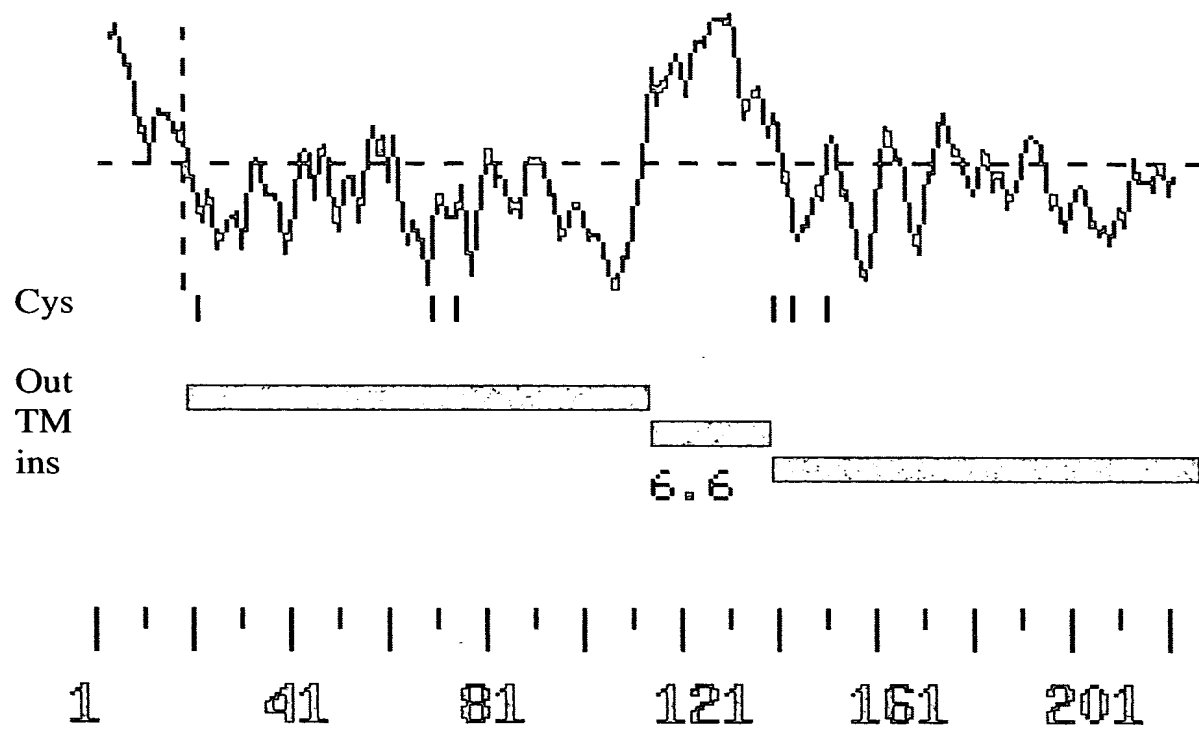
GTCGACCCACGCGTCCGCGGACGCGTGGCGCGCGGGGCCCATCCAGACCCCTGCGGAGAGCGGCCCGGAGCGTCGCC	79
GAGGTTGAGGGCCCGGAGACCGAGGGCCTGGCGGCCGGAAGAACCGCCCCCAAGAGAGCCTCTGGCCCCGGGGGCTGC	158
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> <span>M</span><span>F</span><span>T</span><span>L</span><span>L</span><span>V</span><span>L</span><span>L</span> </div> TGGAACATGTGCGGGGGACACAGTTTGTGTTGACAGTTGCCAGACT ATG TTT ACG CTT CTG GTT CTA CTC	8 228
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> <span>S</span><span>Q</span><span>L</span><span>P</span><span>T</span><span>V</span><span>T</span><span>L</span><span>G</span><span>F</span><span>P</span><span>H</span><span>C</span><span>A</span><span>R</span><span>G</span><span>P</span><span>K</span><span>A</span><span>S</span> </div> AGC CAA CTG CCC ACA GTT ACC CTG GGG TTT CCT CAT TGC GCA AGA GGT CCA AAG GCT TCT	28 288
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> <span>K</span><span>H</span><span>A</span><span>G</span><span>E</span><span>E</span><span>V</span><span>F</span><span>T</span><span>S</span><span>K</span><span>E</span><span>E</span><span>A</span><span>N</span><span>F</span><span>F</span><span>I</span><span>H</span><span>R</span> </div> AAG CAT GCG GGA GAA GAA GTG TTT ACA TCA AAA GAA GAA GCA AAC TTT TTC ATA CAT AGA	48 348
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> <span>R</span><span>L</span><span>L</span><span>Y</span><span>N</span><span>R</span><span>F</span><span>D</span><span>L</span><span>E</span><span>L</span><span>F</span><span>T</span><span>P</span><span>G</span><span>N</span><span>L</span><span>E</span><span>R</span><span>E</span> </div> CGC CTT CTG TAT AAT AGA TTT GAT CTG GAG CTC TTC ACT CCC GGC AAC CTA GAA AGA GAG	68 408
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> <span>C</span><span>N</span><span>E</span><span>E</span><span>L</span><span>C</span><span>N</span><span>Y</span><span>E</span><span>E</span><span>A</span><span>R</span><span>E</span><span>I</span><span>F</span><span>V</span><span>D</span><span>E</span><span>D</span><span>K</span> </div> TGC AAT GAA GAA CTT TGC AAT TAT GAG GAA GCC AGA GAG ATT TTT GTG GAT GAA GAT AAA	88 468
<div style="display: flex; justify-content: space-around; margin-bottom: 5px;"> <span>T</span><span>I</span><span>A</span><span>F</span><span>W</span><span>Q</span><span>E</span><span>Y</span><span>S</span><span>A</span><span>K</span><span>G</span><span>P</span><span>T</span><span>T</span><span>K</span><span>S</span><span>D</span><span>G</span><span>N</span> </div> ACG ATT GCA TTT TGG CAG GAA TAT TCA GCT AAA GGA CCA ACC ACA AAA TCA GAT GGC AAC	108 528

**Fig. 22A**

R	E	K	I	D	V	M	G	L	L	L	T	G	L	I	A	A	G	V	F	L	128
AGA	GAG	AAA	ATA	GAT	GTT	ATG	GGC	CTT	CTG	ACT	GGA	TTA	ATT	GCT	GCT	GGA	GTA	TTT	TTG	588	
V	I	F	G	L	L	G	Y	Y	L	C	I	T	K	C	N	R	L	Q	H	148	
GTT	ATT	TTT	GGA	TTA	CTT	GGC	TAC	TAT	CTT	TGT	ATC	ACT	AAG	TGT	AAT	AGG	CTA	CAA	CAT	648	
P	C	S	S	A	V	Y	E	R	G	R	H	T	P	S	I	I	F	R	R	168	
CCA	TGC	TCT	TCA	GCC	GTC	TAT	GAA	AGG	GGG	AGG	CAC	ACT	CCC	TCC	ATC	ATT	TTC	AGA	AGA	708	
P	E	E	A	A	L	S	P	L	P	P	S	V	E	D	A	G	L	P	S	188	
CCT	GAG	GAG	GCT	GCC	TTG	TCT	CCA	TTG	CCG	CCT	TCT	GTG	GAG	GAT	GCA	GGA	TTA	CCT	TCT	768	
Y	E	Q	A	V	A	L	T	R	K	H	S	V	S	P	P	P	P	Y	P	208	
TAT	GAA	CAG	GCA	GTG	GCG	CTG	ACC	AGA	AAA	CAC	AGT	GTT	TCA	CCA	CCA	CCA	TAT	CCT	828		
G	H	T	K	G	F	R	V	F	K	K	S	M	S	L	P	S	H	*		227	
GGG	CAC	ACA	AAA	GGA	TTT	AGG	GTA	TTT	AAA	AAA	TCT	ATG	TCT	TCT	CTC	CCA	TCT	CAC	TGA	885	
CTACCTTGTCA	TTTGGTATAAGAAA	TTTGTGTTATTTGATAGG	CCGGGCATGGTGGCTCATG	CCCTGTAATCCCAGCAC																964	
TTTGGAGGCCAGGAG	TTTCGAGACCAGCCTGGCCAA	CATGGTGAAACCCGGTCTCTACTAAAAA	ATTCAAAAAATTACCTA	1043																	
GGCGTCATGGGGCATGCCTGTAGT	CCCCACCTACTTGGGAGGCTGAAGCAGGAGA	ATTGCTCGAACCTGGGAGGCAGAGG	1122																		

Fig. 22B





**Fig. 22D**



GTCGACCCAC	CGGTCCGCTG	CGTTCTCACC	CCTGGACCAC	CCTGGGAGAA	CAGTTGACCG	60
AAGTTTGTTT	GGCAGTTGCT	GCTGGACT	ATG TTT CTG	CTT CTG	GTG GTA CTC	112
	Met	Phe	Leu	Leu	Val Val Leu	
	1			5		
AGC CAG CTG	CCC AGA CTT	ACC CTC	GCG GTT	CCT CAT	ACA AGA AGC CTA	160
Ser Gln Leu	Pro Arg Leu	Thr Leu	Ala Val	Pro His	Thr Arg Ser Leu	
	10		15		20	
AAG AAT TCT	GAA CAT GCC	CCA GAA	GGA GTC	TTT GCA	TCA AAA AAA GCA	208
Lys Asn Ser	Glu His Ala	Pro Glu	Gly Val	Phe Ala	Ser Lys Lys Ala	
	25		30		35	
GCA AGC ATC	TTT ATG CAC	CGT CGC	CTC CTA	TAC TAT	AGA TTT GAT TTA	256
Ala Ser Ile	Phe Met His	Arg Arg	Leu Leu	Tyr Asn	Arg Phe Asp Leu	
	45		50		55	
GAA CTC TTC	ACT CCC	GGG AAC	CTG GAG	AGA GAG	TGC TAT GAG GAG TTC	304
Glu Leu Phe	Thr Pro	Gly Asn	Leu Glu	Arg Glu	Cys Tyr Glu Glu Phe	
	60		65		70	
TGT AGT TAT	GAA GAA	GCC AGA	GAG ATC	CTC GGG	GAC AAC GAA GAA ATG	352
Cys Ser Tyr	Glu Glu	Ala Arg	Glu Glu	Ile Leu	Gly Asp Asn Glu Glu Met	
	75		80		85	

**Fig. 22E**

ATC ACA TTC TGG CGG GAA TAT TCA GTC AAA GGA CCA ACC ACA AGA TCA	400
Ile Thr Phe Trp Arg Glu Tyr Ser Val Lys Gly Pro Thr Thr Arg Ser	
90 95 100	
GAT GTC AAC AAA GAG AAA ATT GAT GTT ATG GGC CTT CTG ACT GGC TTA	448
Asp Val Asn Lys Glu Lys Ile Asp Val Met Gly Leu Thr Gly Leu	
105 110 115 120	
ATT GCG GCT GGA GTA TTC TTG GTT GTT TTT GGC TTA CTT GGT TAC TAT	496
Ile Ala Ala Gly Val Phe Leu Val Val Phe Gly Leu Leu Gly Tyr Tyr	
125 130 135	
CTG TGT ATC ACC AAG TGT AAT AGG CAG CCA TAT CAA GGT TCT TCA GCT	544
Leu Cys Ile Thr Lys Cys Asn Arg Gln Pro Tyr Gln Gly Ser Ser Ala	
140 145 150	
GTC TAC ACA AGA AGG ACC AGG CAC ACA CCG TCC ATC ATT TTC AGA ACC	592
Val Tyr Thr Arg Arg Thr Arg His Thr Pro Ser Ile Ile Phe Arg Thr	
155 160 165	
CAT GAG GAA GCT GTC TTG TCT CCA TCG TCA TCC TCA GAG GAC GCG GGA	640
His Glu Glu Ala Val Val Ser Pro Ser Ser Ser Ser Glu Asp Ala Gly	
170 175 180	

**Fig. 22F**

CTA CCT TCC TAT GAA CAG GCA GTA GCT CTG ACC AGA AAA CAC AGT GTC	688
Leu Pro Ser Tyr Glu Gln Ala Val Ala Leu Thr Arg Lys His Ser Val	200
185	
190	
195	
TCA CCA CCA CCT CCA TAT CCT GGG CCA GCA AAA GGA TTT AGG GTA TTT	736
Ser Pro Pro Pro Tyr Pro Gly Pro Ala Lys Gly Phe Arg Val Phe	215
205	
210	
220	
AAA AAG TCA ATG TCA CTC CCA TCT CAC TAAGCCCACC TTGCCGCCCTT	783
Lys Lys Ser Met Ser Leu Pro Ser His	
225	
230	
GCTGTGGTCT GAATAATATG TTCTTCCTGA AACAAACAACA ACAAATAAAT TTGCCCTGTTT	843
AGCTTTTAT GACAAAGCAC AAGGAATAAA GGAACACTAT ATACAGAACA GAATTCACCA	903
CAGCCCCGCT TTCAGCTCTG CCCCCAACTG GATTGCTGTC TTGGTAAGAG ACTTCTACCG	963
TGCTTCCTCG AAGTTAAGAA GAAAGTGCCT TTTTGCAATG TAAACTGTAC TGGTTCAAAC	1023
ATTCTTGCTA CAGTAGGTA CCTATAATCC CCACCTTCAG GAGACTTAGG CGGAGGGAT	1083
GAGAGTTCAA GGCCAGCCTG GGCCCTGTCA GGACGCTGTC TCAAAACAAA GTTTGTTATC	1143
AATAGAATAA TTAGAATTAA CAAACTAGGA TTTTCAGTCT TAAGTCATGA TATTGGATCT	1203
TCTCTTCAGT AAGGTTTCTT TTTGGCTAGA AATACTTCAT AGAAATTTGAC ATTTTGGTAT	1263
ACATCTGTGG CCTTGATACA ATGACTTGAT TTTCTGTTTT AATTAGTGCA GAGGATTCAG	1323
CAAATTGCA GGTCTTCATT TTGTTCCCTC GCTATCCATC GATCATGTTT CAGTGTATTA	1383
AGAGGAGTCA GCCAGGCGTG GTGGCCCCACA CCTGTGATCC CAGCACTTAG GGGGGCATAG	1443
GCAGGCAGAT CTCTGTGAGC TGAAGGACAG CCTGGCCTAC AAAGTCCAGG ACAACCCAGA	1503
CCACACAGAG AAACCTTGTC TTGAAAAACA AAACAAAAAC AAGAGAGAGA GAGAGAGAGA	1563

Fig. 22G

GAGAAAAGAG	ATGTCAAGAG	GTTTTTGTTT	TTTTTTTTTT	AAATTACTAT	TTATGGGCCT	1623
CAC TTGGAAA	AGTGCTTGCC	ATGCAAAATAG	AAGGACAGGA	GTTCAATCCT	CATTACCCAC	1683
ATTTGAAACA	AATAACAAGA	AAAACAACC	AAAAAACCAA	AACAACAAA	ATCTTGAGAA	1743
CTTGAGTGAA	TACCGGTAAC	CTCAGGGCTA	GGCACTGTAA	CTGAATCAGG	AGCCTCCAGA	1803
TCCAGGGAAA	CGCTGTCTCA	ACAAATAAAT	AAATAAGTAA	GTCAGTGAGG	TGGTCTTTAA	1863
ACCCAGCACT	TGAGAGCCAA	AGCAGGGCAG	AGCTCAGTGA	GTTGGAGACC	AGCCTGGTCT	1923
ACAAAGCAAG	TTCTAAGGGA	GCCAGGGCAC	AGAGAAACCC	TGTCGTGAAGG	AAAAAATAAA	1983
AAAAAAAAG	GGCGGCCGC					2002

**Fig. 22H**

G	1	ATGTTTCTGCTTCTGGTGTTACTCAGCCAGCTGCCCAGACTTACCCTCGC	50
H	1	ATGTTTACGCTTCTGGTTCCTACTCAGCCAACTGCCCCACAGTTACCCCTGGG	50
G	51	GGTTCCTCAT...ACAAGAGCCCTAAAGAAATCTGAACATGCCCCAGAAAG	97
H	51	GTTTCCTCATTGCGCAAGAGGTCCAAAGGCTTCTAAGCATGCGGGAGAAG	100
G	98	GAGTCTTTGCATCAAAAAAGCAGCAAGCATCTTTATGCACCGTCGCCCTC	147
H	101	AAGTGTTTACATCAAAAGAGAAAGCAAACTTTTTCATACATAGACGCCCTT	150
G	148	CTATACAATAGATTTGATTAGAACTCTTCACTCCCGGAACCTGGAGAG	197
H	151	CTGTATAATAGATTTGATCTGGAGCTCTTCACTCCCGCAACCTAGAAAG	200
G	198	AGAGTGCTATGAGGAGTTCGTAGTTATGAAGAACCCAGAGAGATCCTCG	247
H	201	AGAGTGCAATGAAGAACCTTGCATTTATGAGGAAGCCAGAGAGATTTTGTG	250

**Fig. 22I**

G	248	GGGACAACGAAAGAAATGATCACATTCCTGGCGGGAATATTCAGTCAAAGGA	297
H	251	TGGATGAAGATAAAACGATTGCATTTTGGCAGGAATATTCAGCTAAAGGA	300
G	298	CCAACCACAAAGATCAGATGTCAACAAGAGAAAAATTGATGTTATGGGCCT	347
H	301	CCAACCACAAAAATCAGATGGCAACAGAGAGAAAAATAGATGTTATGGGCCT	350
G	348	TCTGACTGGCTTAATTGCGGCTGGAGTATTCCTGGTTGTTTGGCTTAC	397
H	351	TCTGACTGGATTAAATTGCTGCTGGAGTATTTTGGTTATTTTGGGATTAC	400
G	398	TTGGTACTATCTGTGTATCACCAAGTGTAATAGGCAGCCATATCAAGGT	447
H	401	TTGGCTACTATCTTTGTATCACTAAGTGTAATAGGCTACAACATCCATGC	450
G	448	TCTTCAGCTGTCTACACAAGAGGACCAGGCACACACCGTCCATCATTTT	497
H	451	TCTTCAGCCGTCTATGAAAGGGG...AGGCACACTCCCTCCATCATTTT	497

**Fig. 22J**

G	498	CAGAACCCATGAGGAAGCTGCTTGTCTCCAT...CGTCATCCTCAGAGG	544
H	498	CAGAAAGACCTGAGGAGGCTGCCTTGTCTCCATTGCCGCCTTCTGTGGAGG	547
G	545	ACGCGGGACTACCTTCCCTATGAACAGGCAGTAGCTCTGACCAGAAAAACAC	594
H	548	ATGCAGGATTACCTTCTTATGAACAGGCAGTGGCGCTGACCAGAAAAACAC	597
G	595	AGTGTCTCACCCACCCTCCATATCCTGGGCCAGCAAAAGGATTTAGGGT	644
H	598	AGTGTTTCACCACCACCACCATATCCTGGGCACACAAAGGATTTAGGGT	647
G	645	ATTTAAAAAGTCAATGTCACCTCCCATCTCAC	675
H	648	ATTTAAAAAATCTATGTCTCTCCCATCTCAC	678

Fig. 22K





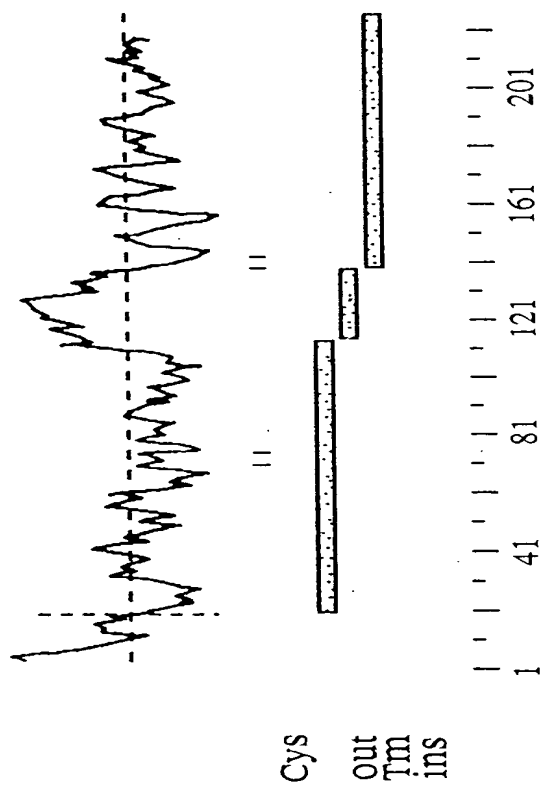


Fig. 22M



T	Y	G	P	D	C	L	A	C	Q	G	G	S	Q	R	P	C	S	G	N	151
ACC	TAC	GGT	CCC	GAC	TGT	CTC	GCA	TGC	CAG	GGC	GGA	TCC	CAG	AGG	CCC	TGC	AGC	GGG	AAT	566
G	H	C	S	G	D	G	S	R	Q	G	D	G	S	C	R	C	H	M	G	171
GGC	CAC	TGC	AGC	GGA	GAT	GGG	AGC	AGA	CAG	GGC	GAC	GGG	TCC	TGC	CGG	TGC	CAC	ATG	GGG	626
Y	Q	G	P	L	C	T	D	C	M	D	G	Y	F	S	S	L	R	N	E	191
TAC	CAG	GGC	CCG	CTG	TGC	ACT	GAC	TGC	ATG	GAC	GGC	TAC	TTC	AGC	TCG	CTC	CGG	AAC	GAG	686
T	H	S	I	C	T	A	C	D	E	S	C	K	T	C	S	G	L	T	N	211
ACC	CAC	AGC	ATC	TGC	ACA	GCC	TGT	GAC	GAG	TCC	TGC	AAG	ACG	TGC	TCG	GGC	CTG	ACC	AAC	746
R	D	C	G	E	C	E	V	G	W	V	L	D	E	G	A	C	V	D	V	231
AGA	GAC	TGC	GGC	GAG	TGT	GAA	GTG	GGC	TGG	GTG	CTG	GAC	GAG	GGC	GCC	TGT	GTG	GAT	GTG	806
D	E	C	A	A	E	P	P	P	C	S	A	A	Q	F	C	K	N	A	N	251
GAC	GAG	TGT	GCG	GCC	GAG	CCG	CCT	CCC	TGC	AGC	GCT	GCG	CAG	TTC	TGT	AAG	AAC	GCC	AAC	866
G	S	Y	T	C	E	E	C	D	S	S	C	V	G	C	T	G	E	G	P	271
GGC	TCC	TAC	ACG	TGC	GAA	GAG	TGT	GAC	TCC	AGC	TGT	GTG	GGC	TGC	ACA	GGG	GAA	GGC	CCA	926
G	N	C	K	E	C	I	S	G	Y	A	R	E	H	G	Q	C	A	D	V	291
GGA	AAC	TGT	AAA	GAG	TGT	ATC	TCT	GGC	TAC	GCG	AGG	GAG	CAC	GGA	CAG	TGT	GCA	GAT	GTG	986

**Fig. 23B**



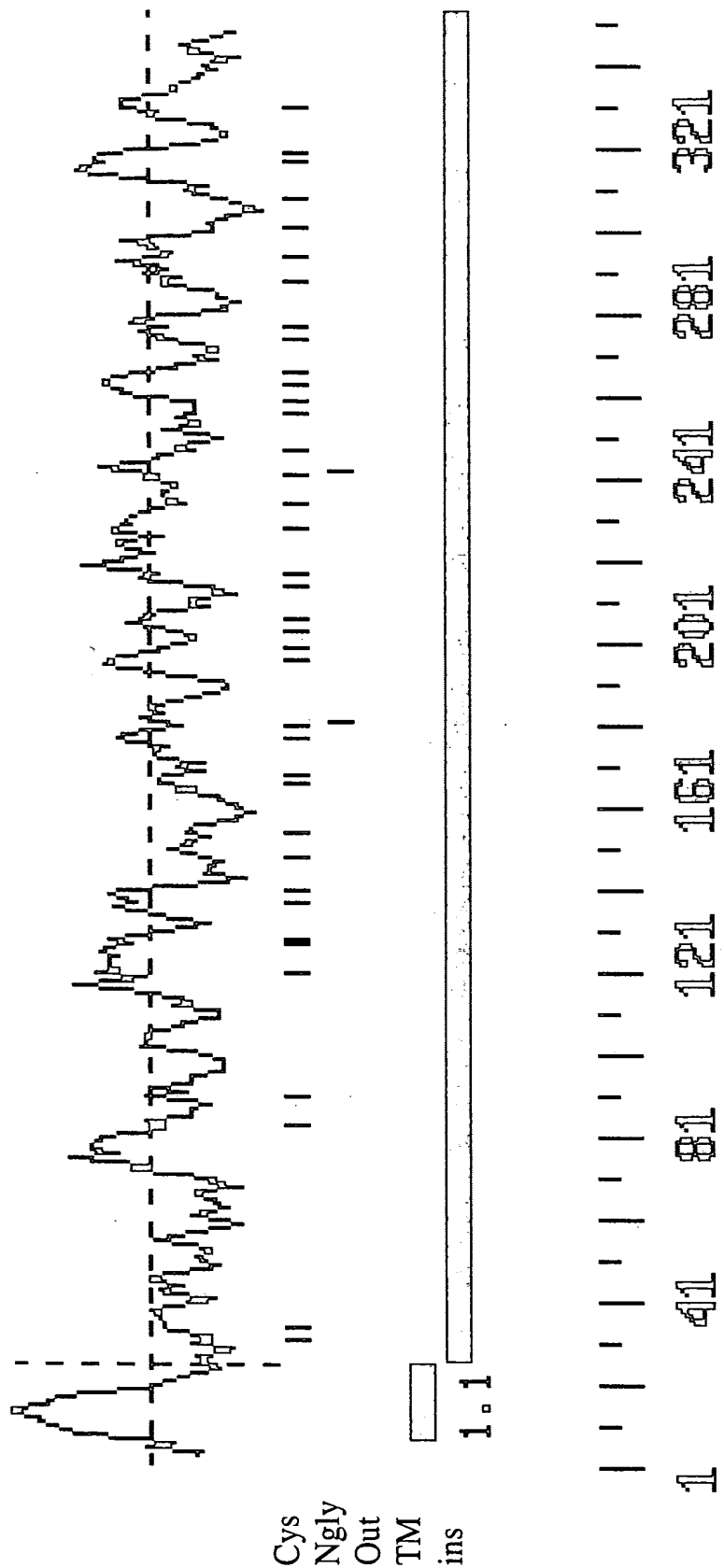


Fig. 23D



```

10      20      30      40      50
C  --GTAGCCGGG--GGAACGGC-CGGC-----GCGCTTG-----CCGGTGGCGGAGGCGGAGACT-CCACA
: . : : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  ACGCGTCCGCACANGGCCGGCGCGGCTGGGAGCGGGTGGGCGGCCGGAGCCGGAGCAGCAGCAGCAGCGCCGCA
10      20      30      40      50      60      70

60      70      80      90      100      110
C  G---CAGTT-CTC-TGCCG-GTCG-CCCGCGAGTGC-ACCCGCCATGCACCTGCCGC-CCGCTGCCGCAG
: . : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  GGACCTGGAGCTCCGGCTGCGTCTTCCCGC-AGCGCTACCCGCCATGCGCCTGCCGCGCGC-GGCCGCGC
80      90      100      110      120      130

120      130      140      150      160      170      180
C  TCGGGCT---GCTACTGCTGCTGCTGCCGCTCCCGCGCGTGCGCTCCCGGAAGCCGACAATGTGCCA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  TGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCGCGCGGAGCGCCCAAGAAGCCGACGCCCTGCCA
140      150      160      170      180      190      200

190      200      210      220      230      240      250
C  GAGGTGCCGGGCGCTGGTGGACAAGTTCAACCAGGGGATGGCCACACAGGCCAGGAAGAAATTCGGCGGC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H  CCGGTGCCGGGCGCTGGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAGAAACTTTGGCGGC
210      220      230      240      250      260      270

```

**Fig. 23F**

```

260      270      280      290      300      310      320
C  GGCAACACGGCGTGGGAGGAGAAGAGTCTGTCCAAAGTACGAATTCAGTGAGATTGGCTCCTGGAGATTA
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  GGGAACACGGCTTGGGAGGAAAGACGCTGTCCAAAGTACGAGTCCAGCGAGATTCCGCTGCTGGAGATCC
280      290      300      310      320      330      340

330      340      350      360      370      380      390
C  TGGAGGGCCTGTGTGACAGCAACGACTTTGAATGCAACCAACT-CTTGGAAACAGCATGAGGAGCAGCTAG
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  TGGAGGGGCTGTGCGAGAGCAGCGACTTCGAAATGCAATCAGATGCTAGAGGC-GCAGGAGGAGCACCTGG
350      360      370      380      390      400      410

400      410      420      430      440      450      460
C  AGGCCCTGGTGGCAGACACTGAAGAAGGAGTGCCCTAACCTATTGAGTGGTTCTGTGTACACACTGAA
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  AGGCCCTGGTGGCTGCAGCTGAAGAGCGGAATATCCTGACTTATTCGAGTGGTTTGTGTGAAGACACTGAA
420      430      440      450      460      470      480

470      480      490      500      510      520      530
C  AGCATGCTGTCTTCCAGGCACCTATGGGCCAGACTGTTCAGGAATGCCAGGTTGGTCTCAGAGGCCCTTGT
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
H  AGTGTGCTGTCTCCAGGAACCTACGGTCCCAGCTGTCTCGCATGCCAGGGCGGATCCCAGAGGCCCTGC
490      500      510      520      530      540      550

```

**Fig. 23G**



```

540      550      560      570      580      590      600
C  AGCGGGAATGGCCACTGCGACGGAGATGGCAGCAGACAGGCGACGGTCTCTGCCAGTGTACGTAGGAT
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
H  AGCGGGAATGGCCACTGCGACGGAGATGGGAGCAGACAGGCGACGGTCTCTGCCGTGCCACATGGGGT
560      570      580      590      600      610      620

610      620      630      640      650      660      670
C  ACAAGGGCCGCTGTGTATCGACTGCATGGATGGCTACTTCAGCTTGCTGAGGAACGAGACCCACAGCTT
   ::::::::::: : :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
H  ACCAGGGCCGCTGTGCACTGCACTGACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCAT
630      640      650      660      670      680      690

680      690      700      710      720      730      740
C  CTGCACAGCCCTGTGATGAGTCCCTGCAAGACATGCTCAGGTCCAACCAACAAGGCTGTGTGGAGTCCGAA
   :::::::::::::: :::::::::::::: :::::::::::::: : :::::::::::::: : ::::::::::::::
H  CTGCACAGCCCTGTGACGAGTCCCTGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAA
700      710      720      730      740      750      760

750      760      770      780      790      800      810
C  GTGGGCTGGACACGTGTGGAGGATGCCCTGTGTGGATGTTGACGAGTGTGCAGCAGACGAGACCCACCCCTGCA
   ::::::::::: . : ::::: :::::::::::::: :::::::::::::: :::::::::::::: : ::::::::::::::
H  GTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGGCCGAGCCGCTCCCTGCA
770      780      790      800      810      820      830

```

**Fig. 23H**

```

      820      830      840      850      860      870      880
C  GCAATGTACAGTACTGTGAAATGTCAACGGCTCCTACACATGTGAAGAGTGTGATTCTACCTGTGTGGG
   :: :: :::::::::::::: :: :::::::::::::: :: :::::::::::::: :: ::::::::::::::
H  GCGCTGCCGAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGG
840      850      860      870      880      890      900

      890      900      910      920      930      940      950
C  CTGCACAGGAAAAGGCCCAATTTGTAAGAGTGTATCTCTGGCTACAGCAAGCAGAAAGGAGAGTGT
   :::::::::::::: :: :::::::::::::: :::::::::::::: :: ::::::::::::::
H  CTGCACAGGGGAAGGCCCAAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGT
910      920      930      940      950      960      970

      960      970      980      990      1000      1010      1020
C  GCAGATATAGATGAATGCTCATTTAGAAACAAGGTGTGTAAGAAAGGAAAAATGAGAACTGCTACAATACTC
   :::::::::::::: :: :: :: :: :::::::::::::: :::::::::::::: ::::::::::::::
H  GCAGATGTGGACGAGTGCTCCTACTAGCAGAAAAAACCTGTGTGAGGAAAAAACGAAACTGCTACAATACTC
980      990      1000      1010      1020      1030      1040

      1030      1040      1050      1060      1070      1080      1090
C  CAGGGAGCTTTTGTCTGCGTGTGTCCGGAAGGTTTCGAGGAAGACAGAAAGATGCTTGTGTACAGACAGCAG
   :::::::::::::: :: :: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
H  CAGGGAGCTACGTCTGTGTGTCTGACGGCTTCGAAAGAA-ACGGAAGATGCCCTGTGTGCCCGCCGCGCAG
1050      1060      1070      1080      1090      1100      1110

```

**Fig. 23I**

```

1100      1110      1120      1130      1140      1150
C AAGCGAAGTGGCAGAGGAAAGT--CCC-ACACAGCCACCCTCCCATGAGGATTGTGACGGGCATCCAG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H AGGCTGAAGCCACAGAAAGGAGAAAGCCCGACACAGCTGCCCTCCCGGAAGA-----CCTG
1120      1130      1140      1150      1160      1170
1160      1170      1180      1190      1200      1210      1220
C GTTCAGAAAGCTGGACTCTCACCCCTTTTAAGTTATTGAGAGGACATCCTATAGAAAAATGTGGCCCATGGAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H --TAATGTGCCGGGACTT--ACCCTTTAAATTATTCAGAAAGGATGTCCCGTGGAAAAATGTGGCCCTGAGGA
1180      1190      1200      1210      1220      1230

1230      1240      1250      1260      1270      1280      1290
C ATCAACCCCATTTCTCCAGGAAGTTTGG-AGGAAGAAGCTGCCTGCTTTGAAACAGTAGATACTCACTT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H TGCCGTCTC---CTGCAGTGGACAGCGGGGAGAGGCTGCCTGCTCTCTAAACGGTTGATTCTCATTT
1240      1250      1260      1270      1280      1290      1300
1300      1310      1320      1330      1340      1350      1360
C GGCCCTTTAAAACGCTGCATTTCTTGGTGGTTCTTAAACAGATTTCGTATATTTTGATACTGTTCTTTATA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H GTCCCTTAAACA-GCTGCATTTCTTGGTGTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCCTTTGTA
1310      1320      1330      1340      1350      1360      1370

1370      1380      1390
C ATAAAATTGATCATTTGAAGGTCACCAGGAA-----CA-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
H ATAAAATTGACCATTGTAGGTAATCAAAAAAAAAAAAAAAAAAGGCGGCCGCTAGAC
1380      1390      1400      1410      1420      1430

```

Fig. 23J

GTCGACCCACGGTCCGTCTCTGGGGCCCCAGCCTCTCTCCTCAGCTCGCGCAGTCTCCGCCGCAGTCTCAGCTGCAGCTG	79
CAGGACTGAGCCCGTGACCCCGGAGGAGACCCCGGAGGAGCGACAAACTTCGCAGTGCCCGCAGACCCAAACCCAGCCCT	158
<div style="text-align: center;">M</div> <div style="display: flex; justify-content: space-around;"> <span>A</span><span>Q</span><span>L</span><span>F</span><span>L</span><span>P</span><span>L</span><span>L</span><span>A</span><span>A</span><span>L</span><span>V</span><span>L</span><span>A</span><span>Q</span> </div> GGTAGCCTGCAGC ATG GCC CAG CTG TTC CTG CCC CTG CTG GCA GCC CTG GTC CTG GCC CAG	16 220
<div style="text-align: center;">A</div> <div style="display: flex; justify-content: space-around;"> <span>P</span><span>A</span><span>A</span><span>L</span><span>A</span><span>D</span><span>V</span><span>L</span><span>E</span><span>G</span><span>D</span><span>S</span><span>S</span><span>E</span><span>D</span><span>R</span><span>A</span><span>F</span><span>R</span> </div> GCT CCT GCA GCT TTA GCA GAT GTT CTG GAA GGA GAC AGC TCA GAG GAC CGC GCT TTT CGC	36 280
<div style="text-align: center;">V</div> <div style="display: flex; justify-content: space-around;"> <span>R</span><span>I</span><span>A</span><span>G</span><span>D</span><span>A</span><span>P</span><span>L</span><span>Q</span><span>G</span><span>V</span><span>L</span><span>G</span><span>G</span><span>A</span><span>L</span><span>T</span><span>I</span><span>P</span> </div> GTG CGC ATC GCG GGC GAC GCG CCA CTG CAG GGC GTG CTC GGC GGC CTC ACC ATC CCT	56 340
<div style="text-align: center;">C</div> <div style="display: flex; justify-content: space-around;"> <span>H</span><span>V</span><span>H</span><span>Y</span><span>L</span><span>R</span><span>P</span><span>P</span><span>P</span><span>S</span><span>R</span><span>R</span><span>A</span><span>V</span><span>L</span><span>G</span><span>S</span><span>P</span><span>R</span> </div> TGC CAC GTC CAC TAC CTG CTG CCG CCA CCG AGC CGC GCT GTG CTG GGC TCT CCG CGG	76 400
<div style="text-align: center;">V</div> <div style="display: flex; justify-content: space-around;"> <span>K</span><span>W</span><span>T</span><span>F</span><span>L</span><span>S</span><span>R</span><span>G</span><span>R</span><span>E</span><span>A</span><span>V</span><span>L</span><span>V</span><span>A</span><span>R</span><span>G</span><span>V</span> </div> GTC AAG TGG ACT TTC CTG TCC CCG GGC CCG GAG GCA GAG GTG CTG GTG GCG GGA GTG	96 460
<div style="text-align: center;">R</div> <div style="display: flex; justify-content: space-around;"> <span>V</span><span>K</span><span>V</span><span>N</span><span>E</span><span>A</span><span>Y</span><span>R</span><span>F</span><span>R</span><span>V</span><span>A</span><span>L</span><span>P</span><span>A</span><span>Y</span><span>P</span><span>A</span><span>S</span> </div> CGC GTC AAG GTG AAC GAG GCG TAC CCG TTC CGC GTG GCA CTG CCT GCG TAC CCA GCG TCG	116 520
<div style="text-align: center;">L</div> <div style="display: flex; justify-content: space-around;"> <span>T</span><span>D</span><span>V</span><span>S</span><span>L</span><span>A</span><span>L</span><span>S</span><span>E</span><span>L</span><span>R</span><span>P</span><span>N</span><span>D</span><span>S</span><span>G</span><span>I</span><span>Y</span><span>R</span> </div> CTC ACC GAC GTC TCC CTG GCG CTG AGC GAG CTG CGC CCC AAC GAC TCA GGT ATC TAT CGC	136 580

Fig. 24A

C	E	V	Q	H	G	I	D	D	S	S	A	V	E	V	K	K	G	156		
TGT	GAG	GTC	CAG	CAC	GAC	ATC	GAT	GAC	AGC	AGC	GCT	GTG	GAG	GTC	AAG	GTC	AAA	GGG	640	
V	V	F	L	Y	R	E	G	S	A	R	Y	A	F	S	F	S	G	A	Q	176
GTC	GTC	TTT	CTC	TAC	CGA	GAG	GGC	TCT	GCC	CGC	TAT	GCT	TTC	TCC	TTT	TCT	GGG	GCC	CAG	700
E	A	C	A	R	I	G	A	H	I	A	T	P	E	Q	L	Y	A	A	Y	196
GAG	GCC	TGT	GCC	CGC	ATT	GGA	GCC	CAC	ATC	GCC	ACC	CCG	GAG	CAG	CTC	TAT	GCC	GCC	TAC	760
L	G	G	Y	E	Q	C	D	A	G	W	L	S	D	Q	T	V	R	Y	P	216
CTT	GGG	GGC	TAT	GAG	CAA	TGT	GAT	GCT	GGC	TGG	CTG	TCG	GAT	CAG	ACC	GTG	AGG	TAT	CCC	820
I	Q	T	P	R	E	A	C	Y	G	D	M	D	G	F	P	G	V	R	N	236
ATC	CAG	ACC	CCA	CGA	GAG	GCC	TGT	TAC	GGA	GAC	ATG	GAT	GGC	TTC	CCC	GGG	GTC	CGG	AAC	880
Y	G	V	V	D	P	D	D	L	Y	D	V	Y	C	Y	A	E	D	L	N	256
TAT	GGT	GTG	GTG	GAC	CCG	GAT	GAC	CTC	TAT	GAT	GTG	TAC	TGT	TAT	GCT	GAA	GAC	CTA	AAT	940
G	E	L	F	L	G	D	P	P	E	K	L	T	L	E	E	A	R	A	Y	276
GGA	GAA	CTG	TTC	CTG	GGT	GAC	CCT	CCA	GAG	AAG	CTG	ACA	TTG	GAG	GAA	GCA	CGG	GCG	TAC	1000
C	Q	E	R	G	A	E	I	A	T	T	G	Q	L	Y	A	A	W	D	G	296
TGC	CAG	GAG	CGG	GGT	GCA	GAG	ATT	GCC	ACC	ACG	GGC	CAA	CTG	TAT	GCA	GCC	TGG	GAT	GGT	1060

**Fig. 24B**

G	L	D	H	C	S	P	G	W	L	A	D	G	S	V	R	Y	P	I	V	316
GGC	CTG	GAC	CAC	TGC	AGC	CCA	GGG	TGG	CTA	GCT	GAT	GGC	AGT	GTG	CGC	TAC	CCC	ATC	GTC	1120
T	P	S	Q	R	C	G	G	G	L	P	G	V	K	T	L	F	L	F	P	336
ACA	CCC	AGC	CAG	CGC	TGT	GGT	GGG	GGC	TTG	CCT	GGT	GTC	AAG	ACT	CTC	TTC	CTC	TTC	CCC	1180
N	Q	T	G	F	P	N	K	H	S	R	F	N	V	Y	C	F	R	D	S	356
AAC	CAG	ACT	GGC	TTC	CCC	AAT	AAG	CAC	AGC	CGC	TTC	AAC	GTC	TAC	TGC	TTC	CGA	GAC	TCG	1240
A	Q	P	S	A	I	P	E	A	S	N	P	A	S	N	P	A	S	D	G	376
GCC	CAG	CCT	TCT	GCC	ATC	CCT	GAG	GCC	TCC	AAC	CCA	GCC	TCC	AAC	CCA	GCC	TCT	GAT	GGA	1300
L	E	A	I	V	T	V	T	E	T	L	E	E	L	Q	L	P	Q	E	A	396
CTA	GAG	GCT	ATC	GTC	ACA	GTG	ACA	GAG	ACC	CTG	GAG	GAA	CTG	CAG	CTG	CCT	CAG	GAA	GCC	1360
T	E	S	E	S	R	G	A	I	Y	S	I	P	I	M	E	D	G	G	G	416
ACA	GAG	AGT	GAA	TCC	CGT	GGG	GCC	ATC	TAC	TCC	ATC	CCC	ATC	ATG	GAG	GAC	GGA	GGA	GGT	1420
G	S	S	T	P	E	D	P	A	E	A	P	R	T	L	L	E	F	E	T	436
GGA	AGC	TCC	ACT	CCA	GAA	GAC	CCA	GCA	GAG	GCC	CCT	AGG	ACG	CTC	CTA	GAA	TTT	GAA	ACA	1480
Q	S	M	V	P	P	T	G	F	S	E	E	E	G	K	A	L	E	E	E	456
CAA	TCC	ATG	GTA	CCG	CCC	ACG	GGG	TTC	TCA	GAA	GAG	GAA	GGT	AAG	GCA	TTG	GAG	GAA	GAA	1540

**Fig. 24C**

E	K	Y	E	D	E	E	E	E	E	E	E	E	V	E	D	476	
GAG	AAA	TAT	GAA	GAT	GAA	GAG	AAA	GAG	GAA	GAA	GAG	GAG	GTG	GAG	GAT	1600	
E	A	L	W	A	W	P	S	E	L	S	S	P	G	P	E	A	496
GAG	GCT	CTG	TGG	GCA	TGG	CCC	AGC	GAG	CTC	AGC	AGC	CCG	GGC	CCT	GAG	GCC	1660
T	E	P	A	A	Q	E	K	S	L	S	Q	A	P	A	R	A	516
ACT	GAG	CCA	GCA	GCC	CAG	CAG	AAG	TCA	CTC	TCC	CAG	GCG	CCA	GCA	AGG	GCA	1720
P	G	A	S	P	L	P	D	G	E	S	E	A	S	R	P	P	536
CCT	GGT	GCA	TCA	CCA	CTT	CCT	GAT	GGA	GAG	TCA	GAA	GCT	TCC	AGG	CCT	CCA	1780
G	P	P	T	E	T	L	P	T	P	R	E	R	N	L	A	S	556
GGA	CCA	CCT	ACT	GAG	ACT	CTG	CCC	ACT	CCC	AGG	GAG	AGG	AAC	CTA	GCA	TCC	1840
S	T	L	V	E	A	A	R	E	V	G	E	A	T	G	G	P	576
TCC	ACT	CTG	GTT	GAG	GCA	AGA	GAG	GAG	GTG	GGG	GAG	GCA	ACT	GGT	GGT	CCT	1900
V	P	R	G	E	S	E	S	E	T	G	S	S	E	G	A	P	596
GTC	CCT	CGA	GGA	GAG	AGC	GAG	GAG	ACA	GGA	AGC	TCC	GAG	GGT	GCC	CCT	TCC	1960
A	T	R	A	P	E	G	T	R	E	L	E	A	P	S	E	D	616
GCC	ACA	CGG	GCC	CCT	GAG	GGT	ACC	AGG	GAG	CTG	GAG	GCC	CCC	TCT	GAA	GAT	2020

**Fig. 24D**

R	T	A	P	A	G	T	S	V	Q	A	Q	P	V	L	P	T	D	S	A	636
AGA	ACT	GCC	CCA	GCA	GGG	ACC	TCA	GTG	CAG	GCC	CAG	CCA	GTG	CTG	CCC	ACT	GAC	AGC	GCC	2080
S	R	G	G	V	A	V	V	P	A	S	G	N	S	A	Q	G	S	T	A	656
AGC	CGA	GGT	GGA	GTG	GCC	GTG	GTC	CCC	GCA	TCA	GGT	AAT	TCT	GCC	CAA	GGC	TCA	ACT	GCC	2140
L	S	I	L	L	L	F	F	P	L	Q	L	W	V	T	*					672
CTC	TCT	ATC	CTA	CTC	CTT	TTC	TTC	CCC	CTG	CAG	CTC	TGG	GTC	ACC	TGA					2188
CCT	GTAG	TCCTT	TAA	CCCC	ACCAT	CAT	CCCC	AACT	CTC	CTGT	CTCTT	TGCC	TTCA	TTCT	TAC	CCAC	CTCT	ACCT	ATGGG	2267
TCT	CCAA	TCT	CGG	ATAT	CCAC	CTT	GTG	GGT	ATCT	CAG	CTCT	CCG	CGT	CTTT	ACC	CTGT	GAT	CCAG	CCCC	2346
CAT	CTGT	GAC	CCCT	TCCC	AT	TGG	GGCC	CTCC	ACCT	GTGG	CTC	ACAT	CTCG	CCAG	CCCC	ACAG	AGCAT	CTC	AGGC	2425
CT	CCAA	GGT	CTC	ATC	ACCT	ATT	GC	AGCC	TT	CAG	GGCT	CGGC	TAT	TTT	CCAC	TACT	CCCT	TCAT	CCGC	2504
GT	CCCC	TTAG	CTGC	CTC	TAT	TGAT	CTC	AGG	GAAG	CCCT	GGG	AGT	CCCT	TTCT	CAC	CCCT	CAAC	CTCC	GGAG	2583
AA	CCCG	TAC	CCCC	CAC	AG	CCCTT	AA	GCA	ACT	ACT	TTCT	GTG	AAG	TAT	TTTT	TGAC	TGTT	TCAT	GGAAA	2662
AA	TAA	ATCT	CTAT	TAA	ACCG	CTTT	GT	AA	CCAAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	GGG	2730

Fig. 24E



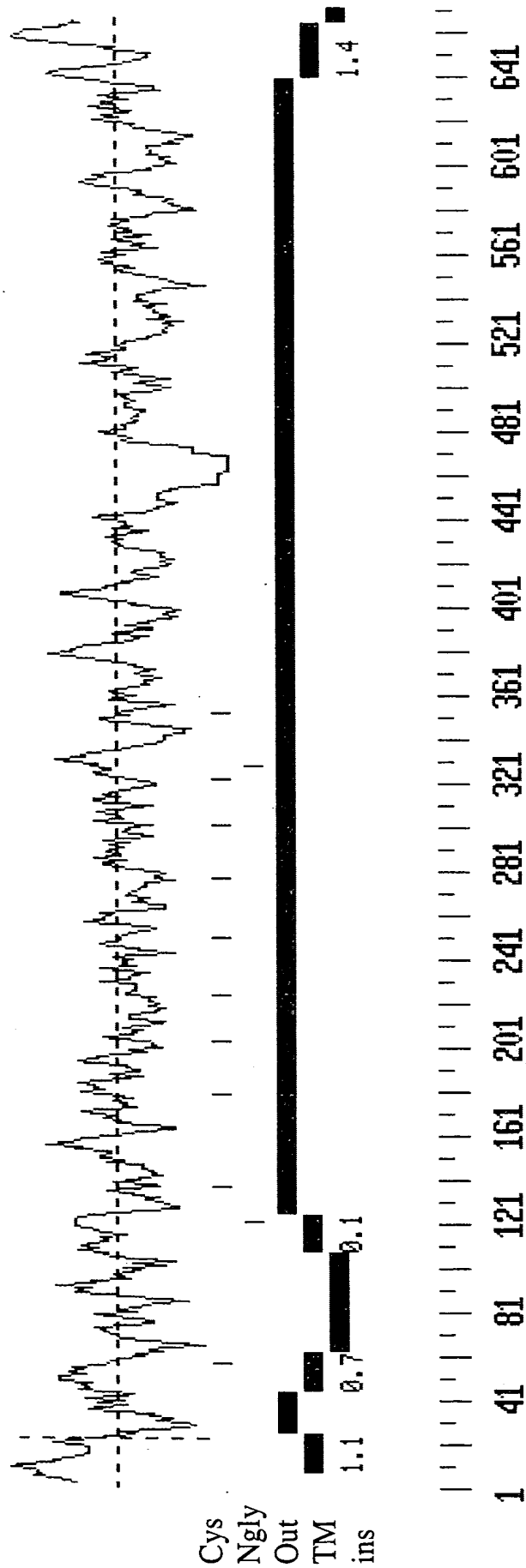


Fig. 24F

10	20	30	40	50	60	70
332	MAQFLPLLAALVLAQAPAAALADVLEGDSS	EDRAFRVRIAGDAPLQGVLGALTIPCHVHVYLRPPPSRRRA				
BEF	MAQFLPLLAALVLAQAPAAALADVLEGDSS	EDRAFRVRIAGDAPLQGVLGALTIPCHVHVYLRPPPSRRRA				
10	20	30	40	50	60	70
332	VLGSPRVKWTFLSRGREA	EVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ				
BEF	VLGSPRVKWTFLSRGREA	EVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ				
150	160	170	180	190	200	210
332	HGIDDSDAVEVKVG	VFLYREGSARYAFSFGAQEACARIGAHIA	TPEQLYAA	YLGGEQCDAGW	LSD	
BEF	HGIDDSDAVE					
220	230	240	250	260	270	280
332	QTVRYPIQTPREACYGDM	DFPGVRNYGVDPDDL	YVYCYAEDLNGELFLGDPPEKLTLEE	ARAYCQER		
BEF	Q--RYPIQTPREACYGDM	DFPGVRNYGVDPDDL	YVYCYAEDLNGELFLGDPPEKLTLEE	ARAYCQER		
290	300	310	320	330	340	350
332	GAEIATTGQLYAAWDGGLD	HCSPGWLADGSVRYPIVTPSQRCGGGLPGVKTLFLFPNQ	TGFFPNKHSR	FNV		
BEF	GAEIATTGQLYAAWDGGLD	HCSPGWLADGSVRYPIVTPSQRCGGGLPGVKTLFLFPNQ	TGFFPNKHSR	FNV		

**Fig. 24G**







680 690 700 710 720 730 740  
M GACYKHFSRRSWEAEQCRALGAHLTSICTPEEQDFVNDRYREYQWIGLNDRTIEGDFLWSDGAPLLY  
H -----SI-----L-----LLF  
:::  
:::  
660

750 760 770 780 790 800 810  
M ENWNPQPDSYFLSGENCVMVWHDQGWSDVPCNYHLSYTCCKMGLVSCGPPQLPLAQIFGRPRLRYAV  
:  
F-----PLQ-----  
:::  
PLQ-----

820 830 840 850 860 870 880  
M DTVLRYRCRDGLAQRNLPLIRCQENGLWEAPQISCVPRRPGRALRSMDAPEGPRGQLSRHRKAPLTPPSS  
:::  
LWVT-----  
670

M L

H -

Fig. 24K

```

10      20      30      40      50
H  GTCG-ACCCA-CG-----CGTCC-----GTCTGGGGCCCCAGCCTCTCTCAGCTCGCGCAGTC
:  :  :::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
M  GAGGCTCCCGCGAGCTGGCGCCCCCTGTCTGGGTCCCGCGCGCCCGGCC-CTGCTCGCGCCCGCGCA-TC
10      20      30      40      50      60

60      70      80      90      100     110     120
H  TCCGCCGAGTCTCAG-CTGCAGCTGCAGGACTGAGCCGTGCACCCGGAGGAGACCCCGGAGAGGCGGA
:  :  :::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
M  GC-GCCGCAGTCTCGGTCTGCGGCTGCGGACGTGACGGCGTGC GCGGAGGGACCTC-----GCAA
70      80      90      100     110     120

130     140     150     160     170     180     190
H  CAAACTTCGAGTGCCCGGACCCCAACCCAGCCCTGGGTAGCCTGCAGCATGGCCCAGCTGTTCTCTGCCC
:  :  :::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
M  -GTTCTTC-----CATC-----AGTG---TGCAGAAATGATACCACCTGCTTCTGTCC
130     140     150     160     170

200     210     220     230     240     250     260
H  CTGCTGGCAGCCCTGGTCTGGCCCAAGCTCCTGCAGCTTTAGCAGATGTTCTGGAAGGAGACAGCTCAG
:  :  :::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
M  CTGCTGGCCGCTCTGGTCTGACCCCAAGCCCTGCCGCCCTCGCTGATGACCTGAAAGAAGACAGCTCGG
180     190     200     210     220     230     240

270     280     290     300     310     320     330
H  AGGACCGCGCTTTTCGGGTGCGCATCGCGGGCGACGCGCCACTGCAGGGCGTGCTCGGGCGGCCCTCAC
:  :  :::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
M  AGGATCGAGCCTTCCGCGTGCATCG-GTGC--CGCGCAGCTGCGGGGCGTGCTGGGCGGTGCCCTGGC
250     260     270     280     290     300

```

**Fig. 24L**

```

340      350      360      370      380      390      400
H CATCCCTTGCCACGTCCACTACCTGCGGCCACCGCCGAGCCGCGGCTGTGCTGGCTCTCCGCGGGTC
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
M CATCCCATGCCACGTCCACCACTGCGGCCCGCGCAGCCGCGGCGCGCGGTTTCCCGGGTC
310      320      330      340      350      360      370

410      420      430      440      450      460      470
H AAGTGGACTTTCCTGTCCCGGGCGGAGGCAGAGGTGCTGGTGGCGGGGAGTGCGCGTCAAGGTGA
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
M AAGTGGACCTTCCTGTCCGGGACCGGAGGTAGAGTTCTGTGGCTCGCGGCTGCGCGTCAAGGTAA
380      390      400      410      420      430      440

480      490      500      510      520      530      540
H ACGAGGCCCTACCGGTTCCGCGTGGCACCTGCCCTGCCAGCGTCGCTACCGACGTCCTCCCTGGCGCT
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
M ACGAAGCCTACCGGTTCCGCGTGCGCTGCCCTACCCCGCATCGCTCACGGATGTGTCTCTAGTATT
450      460      470      480      490      500      510

550      560      570      580      590      600      610
H GAGCGAGCTGCGCCCCAACGACTCAGGTATCTATCGCTGTGAGGTCCAGCACGGCATCGATGACAGCAGC
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
M GAGCGAACTGCGGCCCCAATGATTCCGGGGTCTATCGCTGCGAGGTCCAGCACGGTATCGACGACAGCAGT
520      530      540      550      560      570      580

620      630      640      650      660      670      680
H GACGCTGTGGAGGTCAAGGTCAAAGGGTTCGTCTTTCTCTACCGAGAGGGCTCTGCCCGCTATGCTTTCT
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
M GATGCTGTGGAGGTCAAGGTCAAAGGGTTCGTCTTCTCTACAGAGAGGGCTCTGCGCGCTATGCTTTCT
590      600      610      620      630      640      650

```

**Fig. 24M**



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690      700      710      720      730      740      750
H CCTTTCTGGGGCCAGGAGGCCTGTGCCCGCATTTGGAGCCACATCGCCACCCGGAGAGCTCTATGC
   :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
M CCTTCGCTGGAGCCCAAGGAGCCTGCGCTCGCATAGGAGCCCGAATCGCCACCCCGGAGAGCTCTATGC
660      670      680      690      700      710      720

760      770      780      790      800      810      820
H CGCCTACCTTGGGGCTATGAGCAATGTGATGCTGGCTGGCTCGGATCAGACCGTGAGGTATCCCATC
   :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
M TGCCTACCTCGGCGGCTATGAGCAGTGTGATGCAGGCTGGCTGTCCGACCAAACTGTGAGGTACCCCATC
730      740      750      760      770      780      790

830      840      850      860      870      880      890
H CAGACCCACGAGAGGCCTGTACGGAGACATGGATGGCTTCCCCGGGGTCCGGAACCTATGGTGTGGTGG
   :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
M CAGAACCCACGAGAGGCCTGCTCTGGAGACATGGATGGCTATCCTGGCGTGCGGAACCTACGGAGTGGTGG
800      810      820      830      840      850      860

900      910      920      930      940      950      960
H ACCCGGATGACCTCTATGATGTGTACTGTTATGCTGAAGACCTAAATGGAGAACTGTTCTCTGGGTGACCC
   . :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
M GTCCTGATGATCTCTATGATGTCTACTGTTATGCCGAAGACCTAAATGGAGAACTGTTCTCTAGGCGCCCC
870      880      890      900      910      920      930

970      980      990      1000      1010      1020      1030
H TCCAGAGAAAGCTGACATTGGAGGAAGCACGGGCGTACTGCCAGGAGCGGGGTGCAGAGATTGCCACACAG
   :: . :::::::::::::::::::: : :::::::::::::::::::: : :::::::::::::::::::: :
M TCCCAGCAAGCTGACATGGGAGGAGGCTCGGGACTACTGTCTGGAACGTGGTGCACAGATCGCTAGCACA
940      950      960      970      980      990      1000

```

**Fig. 24N**

	1040	1050	1060	1070	1080	1090	1100
H	GGCCAACTGTATGCAGCCTGGGATGGTGGCCTGGACCACTGCAGCCCAGGGTGCTAGCTAGTGGCAGTG						
M	GGCCAGCTGTACGCAGCCTGGAATGGTGGCCTGGACAGATGTAGCCCTGGCTGGCTGGCTGATGGCAGCG						
	1010	1020	1030	1040	1050	1060	1070
	1110	1120	1130	1140	1150	1160	1170
H	TGCGCTACCCCATCGTCACACCAGCCAGCGCTGTGGTGGGGCTTGCCCTGGTGTCAAGACTCTCTTCCT						
M	TGCGCTATCCCATCATCACACCAGCCAACGCTGTGGGGCGGCCCTGCCAGGAGTCAAGACCCCTCTTCCT						
	1080	1090	1100	1110	1120	1130	1140
	1180	1190	1200	1210	1220	1230	1240
H	CTTCCCCAACAGACTGGCTTCCCCAATAAGCACACAGCCGCTTCAACGTCTACTGCTTCCGAGACTCGGC						
M	CTTTCCCCAACAGACTGGCTTCCCCAGCAAGCAGAACCCTTCAATGTCTACTGCTTCCGAGACTCTGCC						
	1150	1160	1170	1180	1190	1200	1210
	1250	1260	1270	1280	1290	1300	1310
H	CAGCCTTCTGCCATCCCTGAGGCCTCCAACCCAGCCTCCAACCCAGCCTCTGATGGACTAGAGGCTATCG						
M	CATCCCTCTGCTTCCCTCTGAGGCCTCTAGCCCAGCCTC-----AGATGGACTTGAGGCCATTG						
	1220	1230	1240	1250	1260	1270	
	1320	1330	1340	1350	1360	1370	1380
H	TCACAGTGACAGAGACCCCTGGAGGAACCTGCAGCTGCCCTCAGGAAGCCACAGAGAGTGAATCCCCGTGGGC						
M	TCACAGTGACAGAAAAGCTGGAGGAACCTGCAGCTGCCCTCAGGAAGCGATGGAGAGCGAGTCTCGTGGGC						
	1280	1290	1300	1310	1320	1330	1340

**Fig. 240**

[illegible]

**Fig. 24P**

```

1730      1740      1750      1760      1770      1780      1790
H CATCACCACTTCCTGATGGAGAGTCAGAAAGCTTCCAGGCCTCCAAGGTCCATGGACCACCTACTGAGAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CGTCACCTTCTCCTG-----GGCCTCCAAGGTTCCGTGGACCGCCTGCAGAGAC
1670      1680      1690      1700      1710

1800      1810      1820      1830      1840      1850      1860
H TCTGCCCACTCCAGGAGAGGAACCTAGCATCCCCATCACCTTCCACTCTGGTTGAGGCAAGAGAGGTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TTTGCTCCCCCGAGGGAGTGAGC-----GCCACATCTACT-CC----TGGT-GGGGCAAGAGAAAGTA
1720      1730      1740      1750      1760      1770

1870      1880      1890      1900      1910      1920      1930
H GGGGAGGCAACTGGTGGTCCCTGAGCTATCTGGGGTCCCTCGAGGAGAGAGCGAGAGACAGGAAGCTCC-
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGGGGAAACTGGGAGCCCTGAGCTCTCTGGGGTTCTCTCGA---GAGAGCGAGGAGGCGAGGAGCTCCA
1780      1790      1800      1810      1820      1830

1940      1950      1960      1970      1980      1990      2000
H ----GAGGGTGCCCCCTTCCCTGCTTCCAGCCACACGGGCCCCCTGAGGGTACCAGGGAGCTGGAGGCCCC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GCTTGGAGGATGGCCCCCTTCCCTACTTCCAGCTACATGGGCCCCCTGTGGGTCCCAGGGAGCTGGAGACCCC
1840      1850      1860      1870      1880      1890      1900

2010      2020      2030      2040      2050      2060      2070
H CTCTGAAGATAATTCTGGAAGAACTGCCCCAGCAGGGACCTCAGTGCAGGCCCCAGCCAGTGTGCCCCACT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CTCAGAAGAGAGTCTGGAAGAACTGTCTCTGGCAGGCACCTCAGTGCAGGCCCCAGCCAGTGTGCCCCACC
1910      1920      1930      1940      1950      1960      1970

```

**Fig. 24Q**

```

2080      2090      2100      2110      2120      2130
H  GACAGCGCCAGCCGAGGTGGAGTGGCCGTGGTCCCGCATCAGGTAATT-----CTGCCCAAGGCTCA
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GACAGTGCCAGCCACGGTGGAGTGGCTGTGGCTCCCTCATCAGGTGACTGTATCCCCAGGCCCTGCCACA
1980      1990      2000      2010      2020      2030      2040

2140      2150
H  A-----C-TGC-----CCTCT--CTAT-----CCTA-CT-----CCT
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  ATGGTGGACATGCTTGGAGGAGAGGAGGTTTCGCTGCCTATGTTGCCAGGCTATGGGGGGACCT
2050      2060      2070      2080      2090      2100      2110

2160      2170      2180      2190      2200
H  TTTC-----TTCCC--C-----CTGCAGCTCTGG-----GTC--ACCTGA--CCTG----TAGTCCTTT
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GTGCGATGTGGCCCTTCATTTCTGCAGCCCTGGCTGGGAGGCCTTCCAGGAGCCTGCTACAAGCACTTT
2120      2130      2140      2150      2160      2170      2180

2210      2220      2230
H  AACCCAC-----CA-----TCA-TCCCAAACCTCT-----C----CTGTCC----TTT
    . : : : : : : : : : : : : : : : : : : : : : : : : : :
M  TCCACACGAAGGAGTTGGGAGGAGGCAGAAAGTCAGTGCCGAGCGCTAGGTGCTCATCTGACCAGCATCT
2190      2200      2210      2220      2230      2240      2250

2240      2250      2260      2270
H  GC-----CT-----TCATTCTCT-TACCC---ACC---TCTACCTATGGGT-----CTC-----
    : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GCACCCCTGAGGAGCAAGACTTTGTCAATGATCGATACCGGGAGTACCAGTGGATTGGGCTCAATGACAG
2260      2270      2280      2290      2300      2310      2320

```

**Fig. 24R**

```

2280                2290        2300        2310        2320
H  --CAATCTCGGATATCCAC-----CTTGTGG-GTATCTCAGCTCTCCGCGT-CTT-TACCCCTGTG-AT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  GACCATCGAGGGTGACTTCTTGTGGTCAGATGGTGCCCTCTGCTCTATGAAAACTGGAACCCCTGGGCAG
2330      2340      2350      2360      2370      2380      2390

2330                2340                2350
H  CC----CAGC-----CCCGCC-----ACTG-----ACCA---TCTGTGA----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  CCTGACAGCTACTTCCTGTCTCTGGGAGAACTGTGTGGTCATGGTGGCATGACCAGGACAGTGGAGTG
2400      2410      2420      2430      2440      2450      2460

2360      2370      2380                2390
H  ----CCCTTCC-CTGCCATTGGGCC--CTCCA-----CCTGTGG--CTCACATCTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  ATGTGCCCCTGCAACTACCATCTATCCTACACCTGCAAGATGGGGCTTGTGTCTCCTGTGGGCCTC-CACCAC
2470      2480      2490      2500      2510      2520      2530

2400      2410      2420      2430      2440      2450
H  GCCAGCCCCA----CA-----GAGCATCCTCAG---GCCCTCTCCAAGGTCCTCATCACCTATTGCA
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  AGCTACCCCTGGCTCAAATATTGTGTCGCCCTCGGCTGCGCTACGCGGTGGATACTGTGCTTCGATATCG
2540      2550      2560      2570      2580      2590      2600

2460                2470      2480
H  --GCCCTT--CAGG---GCTCGGC-----CTATTTTCCACTAC-----TCC
      : : : . : : : : : : : : : : : : : : : : : : : : : : : : : : :
M  ATGCCGAGACGGGCTGGCTCAGCGCAACCTGCCGTTGATCCGCTGCCAGGAGAAATGGGCTTTGGGAGGCC
2610      2620      2630      2640      2650      2660      2670

```

**Fig. 24S**

```

2490      2500      2510      2520      2530
H CTTCA-TCCGCCGTGTGCC-----GTCC---CCTTTAGCTGC-CTCCT-----ATTGATCTC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CCTCAGATTTCCTGTGTACCCCGGAGGCCTGGCCGTGCTCTGCGCTCCATGGACGCCCCAGAGGACCAC
2680      2690      2700      2710      2720      2730      2740

2540      2550      2560      2570      2580
H AGGGA-AGC-----CTGGGAGTC-CC-TTCTCACC--CCTC-AACCTCCGGAGT-CCAGGAGAAC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGACAGCTCTCGAGGCACAGGAAGCACCCGTTGACACCCGCTCCAGTCTCTAGGAGCCTGGAAAGAC
2750      2760      2770      2780      2790      2800      2810

2590      2600      2610      2620      2630
H CCGTACCCCCA-CAGAGCCTTAA-GCAACTACT-----TCT-----GTGAAGTATTT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M TGCTGCCCCCAGCAGGACCCTCTCACATCAACTGCCAGTGCTCTTCCCCATGATAGGGGTGACGTGAGA
2820      2830      2840      2850      2860      2870      2880

2640      2650
H ----TTGACTGT--TTCA-----TGGAAAACA-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M GGGGTGGGACTGAAAATTTCAGAGGACAGCGCTCGAAGGGGTTTCTTGGGAAAACACTTGGGTGGCTCCGCCCC
2890      2900      2910      2920      2930      2940      2950

2660      2670      2680
H -----AGCCTTGGAAAT-----AAATCTCTATTAA-----AC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M CTCACACAAGGGCCTCAGGTTTACCCCGGTAAGTCCCTAAGTGCCCTCAACTGCCCTCTCATGTCAGCTGC
2960      2970      2980      2990      3000      3010      3020

```

**Fig. 24T**

```

      2690      2700
H  CGCTTTGT-----AAC-----CAAAAAAAAAAAAAAA
  : : : : :
M  CTCCTTGTCCCTCGATNTCGTNAGGGGACACTGTGCTATTTCGATCCTTGATTGTCGAAGAGTTTTAGGAT
3030 3040 3050 3060 3070 3080 3090

      2710      2720      2730
H  AAA-----AAAAAAGGGCG--CC-----GC
  .. : : : : : : : : :
M  GGAGTACCAGCAAAACCAGGTGGAAATAAAGTTGTCTGAACCCCAAAGAAAAAA
3100 3110 3120 3130 3140 3150

```

**Fig. 24U**





G	N	N	P	D	Y	W	K	Y	G	E	A	A	S	T	E	C	N	S	V	191
GG	A	A	A	T	C	C	T	G	A	T	T	G	G	G	G	A	G	A	A	606
C	F	G	D	H	T	Q	P	C	G	G	D	G	R	I	I	L	F	D	T	211
T	G	C	T	T	C	A	A	C	C	C	C	C	C	C	C	C	C	C	C	666
L	V	G	A	C	G	G	N	Y	S	A	M	S	S	V	V	Y	S	P	D	231
C	T	C	G	T	G	G	A	A	T	A	G	A	T	T	T	T	T	T	T	726
F	P	D	T	Y	A	T	G	R	V	C	Y	W	T	I	R	V	P	G	A	251
T	T	C	C	G	A	C	T	A	T	T	T	T	T	T	T	T	T	T	T	786
S	H	I	H	F	S	F	P	L	F	D	I	R	D	S	A	D	M	V	E	271
T	C	C	A	T	C	T	T	C	C	T	A	T	T	T	T	T	T	T	T	846
L	L	D	G	Y	T	H	R	V	L	A	R	F	H	G	R	S	R	P	P	291
C	T	T	G	A	T	A	C	C	A	C	C	T	T	T	T	T	T	T	T	906
L	S	F	N	V	S	L	D	F	V	I	L	Y	F	F	S	D	R	I	N	311
C	T	G	T	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	966
Q	A	Q	G	F	A	V	L	Y	Q	A	V	K	E	E	L	P	Q	E	R	331
C	A	G	C	A	G	A	T	T	A	T	A	T	A	A	G	A	A	A	A	1026

Fig. 25B

P	A	V	N	Q	T	V	A	E	V	I	T	E	Q	A	N	L	S	V	S	351
CCC	GCT	GTC	AAC	CAG	ACG	GTG	GCC	GAG	GTG	ATC	ACG	GAG	CAG	GCC	AAC	CTC	AGT	GTC	AGC	1086
A	A	R	S	S	K	V	L	Y	V	I	T	T	S	P	S	H	P	P	Q	371
GCT	GCC	CGG	TCC	TCC	AAA	GTC	CTC	TAT	GTC	ATC	ACC	ACC	AGC	CCC	AGC	CAC	CCA	CCT	CAG	1146
T	V	P	G	S	N	S	W	A	P	P	M	G	A	G	S	H	R	V	E	391
ACT	GTC	CCA	GGT	AGC	AAT	TCC	TGG	GCG	CCA	CCC	ATG	GGG	GCT	GGA	AGC	CAC	AGA	GTT	GAA	1206
G	W	T	V	Y	G	L	A	T	L	L	I	L	T	V	T	A	I	V	A	411
GGA	TGG	ACA	GTC	TAT	GGT	CTG	GCA	ACT	CTC	CTC	ATC	CTC	ACA	GTC	ACA	GCC	ATT	GTA	GCA	1266
K	I	L	L	H	V	T	F	K	S	H	R	V	P	A	S	G	D	L	R	431
AAG	ATA	CTT	CTG	CAC	GTC	ACA	TTC	AAA	TCC	CAT	CGT	GTT	CCT	GCT	TCA	GGG	GAC	CTT	AGG	1326
D	C	H	Q	P	G	T	S	G	E	I	W	S	I	F	Y	K	P	S	T	451
GAT	TGT	CAT	CAA	CCA	GGG	ACT	TCG	GGG	GAA	ATC	TGG	AGC	ATT	TTT	TAC	AAG	CCT	TCC	ACT	1386
S	I	S	I	F	K	K	K	L	K	G	Q	S	Q	Q	D	D	R	N	P	471
TCA	ATT	TCC	ATC	TTT	AAG	AAG	AAA	CTC	AAG	GGT	CAG	AGT	CAA	CAA	GAT	GAC	CGC	AAT	CCC	1446
L	V	S	D	*																476
CTT	GTG	AGT	GAC	TAA																1461

Fig. 25C

AAACCCCACTGTGCCCTAGGACTTGAGGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGGTTCTTCTC 1540  
TGACAGACTCTTCCCTCCTCTCCCTCTGCCCTCGGCCCTCTTCGGGGAAACCCCTCCTTACAGACTAGGAAGAGGCACCT 1620  
GCTGCCAGGGCAGGCAGAGCCCTGGATTCCCTCCCTGCTT 1657

**Fig. 25D**

GTCGACCCACGGTCCGCGCTCCCGGTGCTCCCGCTGCCCCCTCTGCCCCGGCGCCCGGGGTCCCGCACTGACGGCC															79					
M	A	P	P	A	A	R	L	A	L	L	S	A	A	A	L	T	L	A	19	
C	ATG	GCG	CCG	CCC	GCC	CGT	CTC	GCG	CTG	CTC	TCC	GCC	GCT	GCG	CTC	ACT	CTG	GCG	137	
A	R	P	A	P	G	P	R	S	G	P	E	C	F	T	A	N	G	A	D	39
GCC	CGG	CCC	GCG	CCC	GGT	CCC	CGC	TCC	GGC	CCC	GAG	TGC	TTC	ACA	GCC	AAC	GGT	GCA	GAT	197
Y	R	G	T	Q	S	W	T	A	L	Q	G	G	K	P	C	L	F	W	N	59
TAC	AGG	GGA	ACA	CAG	AGC	TGG	ACA	GCG	CTG	CAA	GGT	GGG	AAG	CCA	TGT	CTG	TTC	TGG	AAC	257
E	T	F	Q	H	P	Y	N	T	L	K	Y	P	N	G	E	G	G	L	G	79
GAG	ACT	TTC	CAG	CAT	CCG	TAC	AAC	ACG	CTG	AAG	TAC	CCC	AAC	GGG	GAA	GGA	GGA	CTG	GGC	317
E	H	N	Y	C	R	N	P	D	G	D	V	S	P	W	C	Y	V	A	E	99
GAG	CAC	AAT	TAT	TGC	AGA	AAT	CCA	GAT	GGA	GAC	GTG	AGC	CCT	TGG	TGC	TAC	GTG	GCC	GAG	377

**Fig. 25E**

H	E	D	G	V	Y	W	K	Y	C	E	I	P	A	C	Q	M	P	G	N	119
CAT	GAG	GAC	GGA	GTC	TAC	TGG	AAG	TAC	TGT	GAA	ATT	CCT	GCC	TGC	CAG	ATG	CCT	GGA	AAC	437
L	G	C	Y	K	D	H	G	N	P	P	P	L	T	G	T	S	K	T	S	139
CTT	GGC	TGC	TAC	AAG	GAT	CAT	GGA	AAC	CCA	CCT	CCT	CTC	ACG	GGC	ACC	AGT	AAA	ACC	TCT	497
N	K	L	T	I	Q	T	C	I	S	F	C	R	S	Q	R	F	K	F	A	159
AAC	AAG	CTC	ACC	ATA	CAA	ACC	TGT	ATC	AGC	TTC	TGT	CGG	AGT	CAG	AGA	TTC	AAG	TTT	GCT	557
G	M	E	S	G	Y	A	C	F	C	G	N	N	P	D	Y	W	K	H	G	179
GGG	ATG	GAG	TCA	GGC	TAT	GCC	TGC	TTC	TGT	GGG	AAC	AAT	CCT	GAC	TAC	TGG	AAG	CAC	GGG	617
E	A	A	S	T	E	C	N	S	V	C	F	G	D	H	T	Q	P	C	G	199
GAG	GCG	GCC	AGC	ACC	GAG	TGC	AAT	AGT	GTC	TGC	TTC	GGG	GAC	CAC	ACG	CAG	CCC	TGC	GGT	677
G	D	G	R	I	I	L	F	D	T	L	V	G	A	C	G	G	N	Y	S	219
GGG	GAC	GGC	AGG	ATT	ATC	CTC	TTT	GAC	ACT	CTC	GTG	GGC	GCC	TGC	GGT	GGG	AAC	TAC	TCA	737
A	M	A	A	V	V	Y	S	P	D	F	P	D	T	Y	A	T	G	R	V	239
GCC	ATG	GCA	GCC	GTG	GTG	TAC	TCC	CCT	GAC	TTC	CCT	GAC	ACC	TAC	GCC	ACT	GGC	AGA	GTC	797
C	Y	W	T	I	R	V	P	G	A	S	R	I	H	F	N	F	T	L	F	259
TGC	TAC	TGG	ACC	ATC	CGG	GTT	CCA	GGA	GCC	TCT	CGC	ATC	CAT	TTC	AAC	TTC	ACC	CTG	TTT	857
D	I	R	D	S	A	D	M	V	E	L	L	D	G	Y	T	H	R	V	L	279
GAT	ATC	AGG	GAC	TCT	GCA	GAC	ATG	GTG	GAG	CTG	CTG	GAC	GGC	TAC	ACC	CAC	CGC	GTC	CTG	917

**Fig. 25F**

V	R	L	S	G	R	S	R	P	P	L	S	F	N	V	S	L	D	F	V	299
GTC	CGG	CTC	AGT	GGG	AGG	AGC	CGC	CCG	CCT	CTG	TCT	TTC	AAT	GTC	TCT	CTG	GAT	TTT	GTC	977
I	L	Y	F	F	S	D	R	I	N	Q	A	Q	G	F	A	V	L	Y	Q	319
ATT	TTG	TAT	TTC	TTC	TCT	GAT	CGC	ATC	AAT	CAG	GCC	CAG	GGA	TTT	GCT	GTG	TTG	TAC	CAA	1037
A	T	K	E	E	P	P	Q	E	R	P	A	V	N	Q	T	L	A	E	V	339
GCC	ACC	AAG	GAG	GAA	CCG	CCA	CAG	GAG	AGA	CCT	GCT	GTC	AAC	CAG	ACC	CTG	GCA	GAG	GTG	1097
I	T	E	Q	A	N	L	S	V	S	A	A	H	S	S	K	V	L	Y	V	359
ATC	ACC	GAG	CAA	GCC	AAC	CTC	AGT	GTC	AGC	GCT	GCC	CAC	TCC	TCC	AAA	GTC	CTC	TAT	GTC	1157
I	T	P	S	P	S	H	P	P	Q	T	A	Q	V	A	I	P	G	H	R	379
ATC	ACC	CCC	AGC	CCC	AGC	CAC	CCT	CCG	CAG	ACT	GCC	CAG	GTA	GCC	ATT	CCT	GGG	CAC	CGT	1217
Q	L	G	P	T	A	T	E	W	K	D	G	L	C	T	A	W	R	P	S	399
CAG	TTG	GGG	CCA	ACA	GCC	ACA	GAG	TGG	AAG	GAT	GGA	CTG	TGT	ACG	GCC	TGG	CGA	CCC	TCC	1277
S	S	S	Q	S	Q	Q	L	S	Q	R	F	F	C	M	S	H	L	N	L	419
TCA	TCC	TCA	CAG	TCA	CAG	CAG	TTG	TCG	CAA	AGA	TTC	TTC	TGC	ATG	TCA	CAT	TTA	AAT	CTC	1337
I	E	S	L	H	Q	E	T	L	G	T	V	V	S	L	G	L	L	E	I	439
ATC	GAG	TCC	CTG	CAT	CAG	GAG	ACC	TTA	GGG	ACT	GTC	GTC	AGC	CTG	GGG	CTT	CTG	GAG	ATA	1397
S	G	P	F	S	M	N	L	P	L	Q	S	P	S	L	R	R	S	S	R	459
TCT	GGA	CCA	TTT	TCT	ATG	AAC	CTT	CCA	CTA	CAA	TCT	CCA	TCT	TTA	AGA	AGA	AGC	TCA	AGG	1457

Fig. 25G

V R V N K M T A I P S \*  
 GTC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG TGA 471  
 1493

GTGACTGAAGCCACGCCCTGCATGAGAGGCTCCGCTCCAAGCTCGAGTTTGCTCCCTGAGTTCTCCTCTGATGAGTTC 1572  
 CCTGCCCTCCCATTCACCAACCATCTCTTTTGGAGACACCCTGCTTTAGAGGCAGCCAGCCTGGGATCCTCCATCACAT 1651  
 GTACCAGCCCTGGCTGCTCTGCTGGGGATGGTAAGACAGGCCCCAGGCTGACAGGACACAGCTGGACCTGACTCCAGAAGA 1730  
 CTCCTGGGTGGTGGGAGGTATAGTGTAGGATGAGTTTCTTCTGCTCTCTCTGTTTGTCCACATACAGATCGGTTTC 1809  
 CCCGTGCTTTACAGTTTGCAATAGAGCCAGACTGAAAGAACTGTCAAGTTTCTAGGCTGGCCTGGTTCCTCCACTAAGA 1888  
 GTGGCAATTGGCGCCCTAGAGGCCACAGAGGCCAGTGTAGGCTTGGAGCTTTCTCTGCTGCCAACTACCATGTGTCACTT 1967  
 AGTCCGAGGGGACTGAGAGCAGGGCCACACCAGATGTCACTTTCTAGAGGGTTCTTTTAGTACCCACTGACCAATGG 2046  
 GGCAAGCCTGAGGATTGGTCCATCTGTTTGTCCATGGAACAGACACAGTGAACCTTCTGGATAC TAGACTTAAC TAGCC 2125  
 TAGCCCTCAAGTAGTTGCCAATCCTGTGGAATCAGAAATTCAGCCTGTCTTCTGTCCTCAGCCCCAAGCCTGTAGCCCTAG 2204  
 AGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCCTTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGC 2283  
 TGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAGCACAGAGCTGG 2362  
 GGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGCTGTAACTCAGCGATCAAGAGCTTGCTTTGTATACATCG 2441  
 GACCCTAGGTTCTATCCAGCACTATCAGAAAGGTGGGAGAGAAAAGACTGCACCATAGCATGCGGGCAGCATCTGTGG 2520  
 TTCCCTACGTGAGGTGTCATCATTTTAAAGCAGATCAAAACTACCCGCGAGTTTGTCCCTTTGTCCCTTATCATGGGAGC 2599  
 AGAGTAGGAGTAAGGGCTCTGGTCTTGCTCATTTGTCCCCAGACAGGGAGGCAAGGAAAGGTCAGGCTTGGAACTGGA 2678  
 GATCCTCCAGGAAAGCTGCAAGATTGAGAGACCCAGCTGCAGTTGGGAGAGGAAGGGCCATCCCCGACTGAGAAAGTC 2757  
 CTGCAGTCTGGAAGTGGCCCTTTGTTCAGCAGCAGCTGTGCCCTGAAGGTAGACCTTGGTCACCTCTCCTGCCAGCCCTTGA 2836  
 GCCCTGCTCTCCTGGGTACCCCTCCTGGAACACCATGCTAACCTTCCCCGAGTCTCTCAGTCACTGCCATTGAGGCCCTC 2915  
 TCCTCTAGCTGCTGTCTCCAGGACTGTCTGGGGCCATCTGGGGATCAGGGAGAGGCAGGAGTACTGACGAGGCCAG 2994  
 TGACCTGAGCTGATGAGTCAACCAGAGGACACCAGAGTCTACAGTGGGCTGGCTGCTGCTCAGCTCCTATGGGAGGCC 3073  
 TACAGGGGTACTAAGCTAGGGGTTCATCTCATTTGATCTGGGAAAGGCTACAGGCTCCTGGATGTGAAGACAGGCC 3152  
 CACTACATAAGAAGACCACCTGGAAATAGACTGACAGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTTCGAGGACTC 3231

Fig. 25H



CCCTGAGACCAAGTGTGAGTCACAGAGTGCCATGTGCGTAGTGCAATAAAGGATATGGGTTCTTAACCCAGGGAAGGCTC 3310  
 ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACCTCACCTGTCTCTTCCCT 3389  
 ATCTCGGACACAGGAAGCAAGCCCAAGTGTGGTGGCAGCTGCGGCTCAGCATTTGGTGTCCCCAGGAAGGCGGTGGATG 3468  
 TGCCACGCTCCTTTTGTCTGTGGCCTGGCACAGCCCAACACTGCAGGGCCCACTTCTCTCTTGGGGGTAGGGACAC 3547  
 ATAAGGAATAAATAACCCACCTCCAACAACAGCAGAGAGACAGTGGGAAGGAAGGCTGTAAATCACCCAGGCCAGACCTC 3626  
 CAGAAATGACAGGCACAGTCTGTAGAACCTGTAGGCAGCCCTCAGAGACATCAGCTAAATAAATAGTGCCCTATGTCCCTCCCT 3705  
 GAGCATAGGGGTAAAGCCGAGGGAAGAGCAGCCCTCAGAGACATCAGCTAAATAAATAGTGCCCTATGTCCCTCCCT 3784  
 TCCTGTACACTGCTTACAAAGCAGAGACAGAGTGTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA 3863  
 GCGGCTGCCCTAAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGCTCTGGCTTCAGACTCCTCAGCCA 3942  
 AAAGCTCTTGAAAGATCAAGCTCTGGCGGGTACAGCTGTCTGGCCTGTGGCCAGCCCATGGGATGTGCCGTGGGCCAG 4021  
 GTGCCACCCACGGCTCACTGTCTATCCAGGAGGACCCACCTGATGCTCCTCATCATCCGCTGGCTTGACACTATCA 4100  
 GAGCTCGCGCGGCTGTGCCAGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGGATGGCCTCCAGA 4179  
 CTCGTGTCAGCCCTCTGCAGGGCCACACAAGTCTCCCGAGCCAAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCCT 4258  
 GTGGAGTGTCCCTGTTGATGTCTGAGGTCGTGCTTTGGGTACCCGCCCTGGGAACCTGCTAACCTCCGATTGGTCCCTTTGT 4337  
 GTCCTCTGTTTACTGTCCCTCTTCTACCTCCAGGTCACTTAGCTCTGGCTGTCTGGCTGGGAGTGGGGGTGGGGATGCT 4416  
 GGCTGCACCCCAACCTGGTCTGCCAACAGAACCTGGGGGCTCACACGGGCTCCTGTCTTGCCAAAGCTGGAGCTGAGC 4495  
 AACTGGCCCAAGGCTGAGTGGGGCAGAGCAAAACAAGTGGGAAGGGATCTCTCTCCTTAGAGGGAGGTGCCGGAAGGTGT 4574  
 AGATCCAGCGAGGAGCTGCCATCCCCGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAAATCTCACCTCCAGCAG 4653  
 GGATATGACTTTGGACACAAGGCTTTATTTGTAAATATGCTCTTAATAATGCAACTTTTGAGAAATAAGATAGAAACATCA 4732  
 TGTAATTTTAAATAATAAAATGAAGTGTGACACACTGTATACAATTTAATATATATATTTTAGGATTTTGTATTAAAGAA 4811  
 AATGGAATGTGATGGTACTTAACCTTTTACAAAAGAGAGAAAATGTTATTTTACTGTTTGAAAGAAAATAAATATTCTCA 4890  
 TTGTTGTAGAAAAAATAAAAAAAGGGGCGCGC 4928

**Fig. 25I**

Hum.	MAPPAARLALLSAAALTLAARPAPSPGLGPGPECF	TANGADYRG	TQNW	TALQG	KPCLFW	NETFQHP	YNT
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::
Mur.	MAPPAARLALLSAAALTLAARPAPGPR--SG	PECF	TANGADYRG	TQSW	TALQG	KPCLFW	NETFQHP
	10	20	30	40	50	60	
Hum.	LKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWKYCEI	PACQ	MPGN	LG	CYKDHGN	PPPLT	GT
	80	90	100	110	120	130	140
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::
Mur.	LKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWKYCEI	PACQ	MPGN	LG	CYKDHGN	PPPLT	GT
	70	80	90	100	110	120	130
Hum.	SNKLTIQTCISFCRSQRFK	FAGMESGYACFCGN	NP	DYWKYGEAA	STECNSV	CFGDHTQ	PCGGDGR
	150	160	170	180	190	200	210
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::
Mur.	SNKLTIQTCISFCRSQRFK	FAGMESGYACFCGN	NP	DYWKYGEAA	STECNSV	CFGDHTQ	PCGGDGR
	140	150	160	170	180	190	200
Hum.	TLVGACGGNYSAMSSV	VYSPDFPD	TYATGRVCYWT	IRVPGASHIH	FSFPL	FDIRDSAD	MVELLDGY
	220	230	240	250	260	270	280
	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::	::::::::::::::::::::
Mur.	TLVGACGGNYSAMAAV	VYSPDFPD	TYATGRVCYWT	IRVPGASRIH	FNFTL	FDIRDSAD	MVELLDGY
	210	220	230	240	250	260	270

Hum.	LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQAVKEELPQERPAVNQTVAEVITEQANLSV	290	300	310	320	330	340	350
Mur.	LVRLSGRSRPPLSFNVSLDFVILYFFSDRINQAQGFVLYQATKEEPPQERPAVNQTLAEVITEQANLSV	280	290	300	310	320	330	340
Hum.	SAARSSKVLVITTPSPHPPTVPGSNSWAPPMGAGSHRVEGWTVYGLATLLILTVTAIVAKILLHVTFK	360	370	380	390	400	410	420
Mur.	SAAHSSKVLVITTPSPHPPTAQVAIPGHRQLGPTA---TEWKD-GLCTAWRPSSSSQSQLSQRFECM	350	360	370	380	390	400	410
Hum.	SHRVPASGDLRDCHQPGTSGEIWISIFYKPPSTISIFKKKLKGQSQ-QDDRNPLVSD	430	440	450	460	470		
Mur.	SHLNLIESHQETLGTVVSGLGLEISGPFMSMNLPLQSPSLRRSSRVNVNKMTAIPS	420	430	440	450	460	470	

**Fig. 25K**

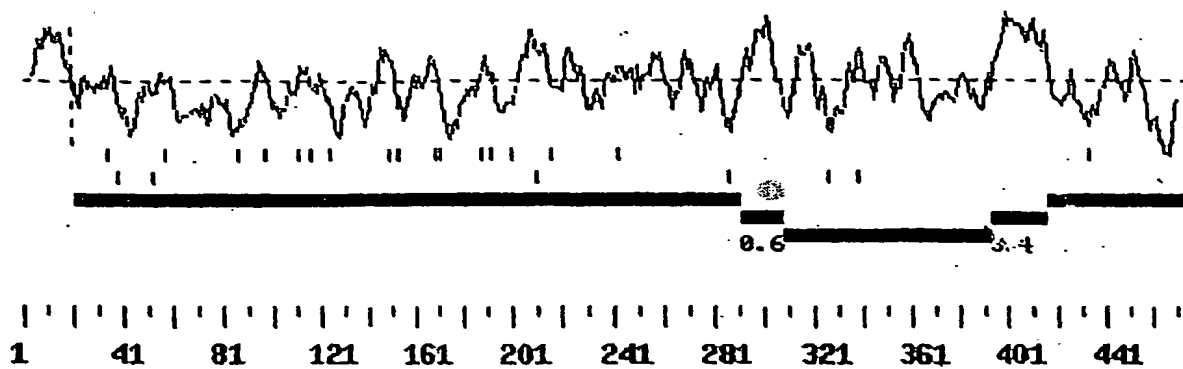


Fig 25L

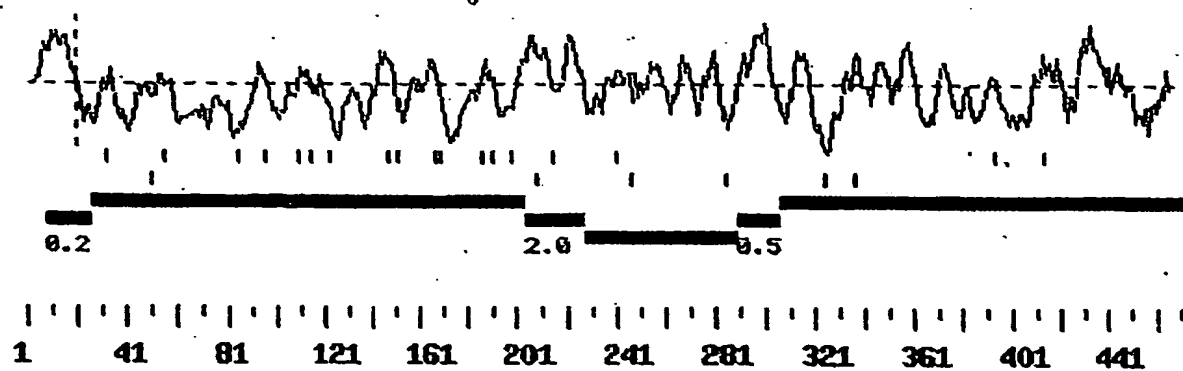


Fig. 25M

GCGGCCGCTCGCGATCTAGAACTAGTA	M	M	L	P	Q	N	S	W	H	I	D	F	G	13
	ATG	ATG	CTG	CCT	CAA	AAC	TCG	TGG	CAT	ATT	GAT	TTT	GGA	66
R C C C H Q N L F S A V T C I L L L N														33
AGA TGC TGC TGT CAT CAG AAC CTT TTC TCT GCT GGT GTG GTA ACT TGC ATC CTG CTC CTG AAT														126
S C F L I S S F N G T D L E L R L V N G														53
TCC TGC TTT CTC ATC AGC AGT TTT AAT GGA ACA GAT TTG GAG TTG AGG CTG GTC AAT GGA														186
D G P C S G T V E V K F Q G Q W G T V C														73
GAC GGT CCC TGC TCT GGG ACA GTG GAG GTG AAA TTC CAG GGA CAG TGG GGG ACT GTG TGT														246
D D G W N T T A S T V V C K Q L G C P F														93
GAT GAT GGG TGG AAC ACT ACT GCC TCA ACT GTC GTG TGC AAA CAG CTT GGA TGT CCA TTT														306
S F A M F R F G Q Q A V T R H G K I W L D														113
TCT TTC GCC ATG TTT CGT TTT GGA CAA GCC GTG ACT AGA CAT GGA AAA ATT TGG CTT GAT														366
D V S C Y G N E S A L W E C Q H R E W G														133
GAT GTT TCC TGT TAT GGA AAT GAG TCA GCT CTC TGG GAA TGT CAA CAC CGG GAA TGG GGA														426
S H N C Y H G E D V G V N C Y G E A N L														153
AGC CAT AAC TGT TAT CAT GGA GAA GAT GTT GGT GTG AAC TGT TAT GGT GAA GCC AAT CTG														486

**Fig. 26A**

G	L	R	L	V	D	G	N	N	S	C	S	G	R	V	E	V	K	F	Q	173
GGT	TTG	AGG	CTA	GTG	GAT	GGA	AAC	AAC	TCC	TGT	TCA	GGG	AGA	GTG	GAG	GTG	AAA	TTC	CAA	546
E	R	W	G	T	I	C	D	D	G	W	N	L	N	T	A	A	V	V	C	193
GAA	AGG	TGG	GGG	ACT	ATA	TGT	GAT	GAT	GGG	TGG	AAC	TTG	AAT	ACT	GCT	GCC	GTG	GTG	TGC	606
R	Q	L	G	C	P	S	S	F	I	S	S	G	V	V	N	S	P	A	V	213
AGG	CAA	CTA	GGA	TGT	CCA	TCT	TCT	TTT	ATT	TCT	TCT	GGA	GTT	GTT	AAT	AGC	CCT	GCT	GTA	666
L	R	P	I	W	L	D	D	I	L	C	Q	G	N	E	L	A	L	W	N	233
TTG	CGC	CCC	ATT	TGG	CTG	GAT	GAC	ATT	TTA	TGC	CAG	GGG	AAT	GAG	TTG	GCA	CTC	TGG	AAT	726
C	R	H	R	G	W	G	N	H	D	C	S	H	N	E	D	V	T	L	T	253
TGC	AGA	CAT	CGT	GGA	TGG	GGA	AAT	CAT	GAC	TGC	AGT	CAC	AAT	GAG	GAT	GTC	ACA	TTA	ACT	786
C	Y	D	S	S	D	L	E	L	R	L	V	G	G	T	N	R	C	M	G	273
TGT	TAT	GAT	AGT	AGT	GAT	CTT	GAA	CTA	AGG	CTT	GTA	GGT	GGA	ACT	AAC	CGC	TGT	ATG	GGG	846
R	V	E	L	K	I	Q	G	R	W	G	T	V	C	H	H	K	W	N	N	293
AGA	GTA	GAG	CTG	AAA	ATC	CAA	GGA	AGG	TGG	GGG	ACC	GTA	TGC	CAC	CAT	AAG	TGG	AAC	AAT	906
A	A	A	D	V	V	C	K	Q	L	G	C	G	T	A	L	H	F	A	G	313
GCT	GCA	GCT	GAT	GTC	GTA	TGC	AAG	CAG	TTG	GGA	TGT	GGA	ACC	GCA	CTT	CAC	TTC	GCT	GGC	966
L	P	H	L	Q	S	G	S	D	V	V	W	L	D	G	V	S	C	S	G	333
TTG	CCT	CAT	TTG	CAG	TCA	GGG	TCT	GAT	GTT	GTA	TGG	CTT	GAT	GGT	GTC	TCC	TGC	TCC	GGT	1026

**Fig. 26B**

N	E	S	F	L	W	D	C	R	H	S	G	T	V	N	F	D	C	L	H	353
AAT	GAA	TCT	TTT	CTT	TGG	GAC	TGC	AGA	CAT	TCC	GGA	ACC	GTC	AAT	TTT	GAC	TGT	CTT	CAT	1086
Q	N	D	V	S	V	I	C	S	D	G	A	D	L	E	L	R	L	A	D	373
CAA	AAC	GAT	GTG	TCT	GTG	ATC	TGC	TCA	GAT	GGA	GCA	GAT	TTG	GAA	CTG	CGA	CTA	GCA	GAT	1146
G	S	N	N	C	S	G	R	V	E	V	R	I	H	E	Q	W	W	T	I	393
GGA	AGT	AAC	AAT	TGT	TCA	GGG	AGA	GTA	GAG	GTG	AGA	ATT	CAT	GAA	CAG	TGG	TGG	ACA	ATA	1206
C	D	Q	N	W	K	N	E	Q	A	L	V	V	C	K	Q	L	G	C	P	413
TGT	GAC	CAG	AAC	TGG	AAG	AAT	GAA	CAA	GCC	CTT	GTG	GTT	TGT	AAG	CAG	CTA	GGA	TGT	CCG	1266
F	S	V	F	G	S	R	R	A	K	P	S	N	E	A	R	D	I	W	I	433
TTC	AGC	GTC	TTT	GGC	AGT	CGT	CGT	GCT	AAA	CCT	AGT	AAT	GAA	GCT	AGA	GAC	ATT	TGG	ATA	1326
N	S	I	S	C	T	G	N	E	S	A	L	W	D	C	T	Y	D	G	K	453
AAC	AGC	ATA	TCT	TGC	ACT	GGG	AAT	GAG	TCA	GCT	CTC	TGG	GAC	TGC	ACA	TAT	GAT	GGA	AAA	1386
A	K	R	T	C	F	R	R	S	D	A	G	V	I	C	S	D	K	A	D	473
GCA	AAG	CGA	ACA	TGC	TTC	CGA	AGA	TCA	GAT	GCT	GGA	GTA	ATT	TGT	TCT	GAT	AAG	GCA	GAT	1446
L	D	L	R	L	V	G	A	H	S	P	C	Y	G	R	L	E	V	K	Y	493
CTG	GAC	CTA	AGG	CTT	GTC	GGG	GCT	CAT	AGC	CCC	TGT	TAT	GGG	AGA	TTG	GAG	GTG	AAA	TAC	1506
Q	G	E	W	G	T	V	C	H	D	R	W	S	T	R	N	A	A	V	V	513
CAA	GGA	GAG	TGG	GGG	ACT	GTG	TGT	CAT	GAC	AGA	TGG	AGC	ACA	AGG	AAT	GCA	GCT	GTT	GTG	1566

**Fig. 26C**

C	K	Q	L	G	C	G	K	P	M	H	V	F	G	M	T	Y	F	K	E	533
TGT	AAA	CAA	TTG	GGA	TGT	GGA	AAG	CCT	ATG	CAT	GTG	TTT	GGT	ATG	ACC	TAT	TTT	AAA	GAA	1626
A	S	G	P	I	W	L	D	D	V	S	C	I	G	N	E	S	N	I	W	553
GCA	TCA	GGA	CCT	ATT	TGG	CTG	GAT	GAC	GTT	TCT	TGC	ATT	GGA	AAT	GAG	TCA	AAT	ATC	TGG	1686
D	C	E	H	S	G	W	G	K	H	N	C	V	H	R	E	D	V	I	V	573
GAC	TGT	GAA	CAC	AGT	GGA	TGG	GGA	AAG	CAT	AAT	TGT	GTA	CAC	AGA	GAG	GAT	GTG	ATT	GTA	1746
T	C	S	G	D	A	T	W	G	L	R	L	V	G	G	S	N	R	C	S	593
ACC	TGC	TCA	GGT	GAT	GCA	ACA	TGG	GGC	CTG	AGG	CTG	GTG	GGC	GGC	AGC	AAC	CGC	TGC	TCG	1806
G	R	L	E	V	Y	F	Q	G	R	W	G	T	V	C	D	D	G	W	N	613
GGA	AGA	CTG	GAG	GTG	TAC	TTT	CAA	GGA	CGG	TGG	GGC	ACA	GTG	TGT	GAT	GAC	GGC	TGG	AAC	1866
S	K	A	A	A	V	V	C	S	Q	L	D	C	P	S	S	I	I	G	M	633
AGT	AAA	GCT	GCA	GCT	GTG	GTG	TGT	AGC	CAG	CTG	GAC	TGC	CCA	TCT	TCT	ATC	ATT	GGC	ATG	1926
G	L	G	N	A	S	T	G	Y	G	K	I	W	L	D	D	V	S	C	D	653
GGT	CTG	GGA	AAC	GCT	TCT	ACA	GGA	TAT	GGA	AAA	ATT	TGG	CTC	GAT	GAT	GTT	TCC	TGT	GAT	1986
G	D	E	S	D	L	W	S	C	R	N	S	G	W	G	N	N	D	C	S	673
GGA	GAT	GAG	TCA	GAT	CTC	TGG	TCA	TGC	AGG	AAC	AGT	GGG	TGG	GGA	AAT	AAT	GAC	TGC	AGT	2046
H	S	E	D	V	G	V	I	C	S	D	A	S	D	M	E	L	R	L	V	693
CAC	AGT	GAA	GAT	GTT	GGA	GTG	ATC	TGT	TCT	GAT	GCA	TCG	GAT	ATG	GAG	CTG	AGG	CTT	GTG	2106

**Fig. 26D**



G	G	S	S	R	C	A	G	K	V	E	V	N	V	Q	G	A	V	G	I	713
GGT	GGA	AGC	AGC	AGG	TGT	GCT	GGA	AAA	GTT	GAG	GTG	AAT	GTC	CAG	GGT	GCC	GTG	GGA	ATT	2166
L	C	A	N	G	W	G	M	N	I	A	E	V	V	C	R	Q	L	E	C	733
CTG	TGT	GCT	AAT	GGC	TGG	GGA	ATG	AAC	ATT	GCT	GAA	GTT	GTT	TGC	AGG	CAA	CTT	GAA	TGT	2226
G	S	A	I	R	V	S	R	E	P	H	F	T	E	R	T	L	H	I	L	753
GGG	TCT	GCA	ATC	AGG	GTC	TCC	AGA	GAG	CCT	CAT	TTC	ACA	GAA	AGA	ACA	TTA	CAC	ATC	TTA	2286
M	S	N	S	G	C	T	G	G	E	A	S	L	W	D	C	I	R	W	E	773
ATG	TCG	AAT	TCT	GGC	TGC	ACT	GGA	GGG	GAA	GCC	TCT	CTC	TGG	GAT	TGT	ATA	CGA	TGG	GAG	2346
W	K	Q	T	A	C	H	L	N	M	E	A	S	L	I	C	S	A	H	R	793
TGG	AAA	CAG	ACT	GCG	TGT	CAT	TTA	AAT	ATG	GAA	GCA	AGT	TTG	ATC	TGC	TCA	GCC	CAC	AGG	2406
Q	P	R	L	V	G	A	D	M	P	C	S	G	R	V	E	V	K	H	A	813
CAG	CCC	AGG	CTG	GTT	GGA	GCT	GAT	ATG	CCC	TGC	TCT	GGA	CGT	GTT	GAA	GTG	AAA	CAT	GCA	2466
D	T	W	R	S	V	C	D	S	D	F	S	L	H	A	A	N	V	L	C	833
GAC	ACA	TGG	CGC	TCT	GTC	TGT	GAT	TCT	GAT	TTC	TCT	CTT	CAT	GCT	GCC	AAT	GTG	CTG	TGC	2526
R	E	L	N	C	G	D	A	I	S	L	S	V	G	D	H	F	G	K	G	853
AGA	GAA	TTA	AAT	TGT	GGA	GAT	GCC	ATA	TCT	CTT	TCT	GTG	GGA	GAT	CAC	TTT	GGA	AAA	GGG	2586
N	G	L	T	W	A	E	K	F	Q	C	E	G	S	E	T	H	L	A	L	873
AAT	GGT	CTA	ACT	TGG	GCC	GAA	AAG	TTC	CAG	TGT	GAA	GGG	AGT	GAA	ACT	CAC	CTT	GCA	TTA	2646

**Fig. 26E**

C	P	I	V	Q	H	P	E	D	T	C	I	H	S	R	E	V	G	V	893	
TGC	CCC	ATT	GTT	CAA	CAT	CCG	GAA	GAC	ACT	TGT	ATC	CAC	AGC	AGA	GAA	GTT	GGA	GTT	GTC	2706
C	S	R	Y	T	D	V	R	L	V	N	G	K	S	Q	C	D	G	Q	V	913
TGT	TCC	CGA	TAT	ACA	GAT	GTC	CGA	CTT	GTG	AAT	GGC	AAA	TCC	CAG	TGT	GAC	GGG	CAA	GTG	2766
E	I	N	V	L	G	H	W	G	S	L	C	D	T	H	W	D	P	E	D	933
GAG	ATC	AAC	GTG	CTT	GGA	CAC	TGG	GGC	TCA	CTG	TGT	GAC	ACC	CAC	TGG	GAC	CCA	GAA	GAT	2826
A	R	V	L	C	R	Q	L	S	C	G	T	A	L	S	T	T	G	G	K	953
GCC	CGT	GTT	CTA	TGC	AGA	CAG	CTC	AGC	TGT	GGG	ACT	GCT	CTC	TCA	ACC	ACA	GGA	GGA	AAA	2886
Y	I	G	E	R	S	V	R	V	W	G	H	R	F	H	C	L	G	N	E	973
TAT	ATT	GGA	GAA	AGA	AGT	GTT	CGT	GTG	TGG	GGA	CAC	AGG	TTT	CAT	TGC	TTA	GGG	AAT	GAG	2946
S	L	L	D	N	C	Q	M	T	V	L	G	A	P	P	C	I	H	G	N	993
TCA	CTT	CTG	GAT	AAC	TGT	CAA	ATG	ACA	GTT	CTT	GGA	GCA	CCT	CCC	TGT	ATC	CAT	GGA	AAT	3006
T	V	S	V	I	C	T	G	S	L	T	Q	P	L	F	P	C	L	A	N	1013
ACT	GTC	TCT	GTG	ATC	TGC	ACA	GGA	AGC	CTG	ACC	CAG	CCA	CTG	TTT	CCA	TGC	CTC	GCA	AAT	3066
V	S	D	P	Y	L	S	A	V	P	E	G	S	A	L	I	C	L	E	D	1033
GTA	TCT	GAC	CCA	TAT	TTG	TCT	GCA	GTT	CCA	GAG	GGC	AGT	GCT	TTG	ATC	TGC	TTA	GAG	GAC	3126
K	R	L	R	L	V	D	G	D	S	R	C	A	G	R	V	E	I	Y	H	1053
AAA	CGG	CTC	CGC	CTA	GTG	GAT	GGG	GAC	AGC	CGC	TGT	GCC	GGG	AGA	GTA	GAG	ATC	TAT	CAC	3186

**Fig. 26F**

D	G	F	W	G	T	I	C	D	D	G	W	D	L	S	D	A	H	V	V	1073
GAC	GGC	TTC	TGG	GGC	ACC	ATC	TGT	GAT	GAC	GGC	TGG	GAC	CTG	AGC	GAT	GCC	CAC	GTG	GTG	3246
C	Q	K	L	G	C	G	V	A	F	N	A	T	V	S	A	H	F	G	E	1093
TGT	CAA	AAG	CTG	GGC	TGT	GGA	GTG	GCC	TTC	AAT	GCC	ACG	GTC	TCT	GCT	CAC	TTT	GGG	GAG	3306
G	S	G	P	I	W	L	D	D	L	N	C	T	G	T	E	S	H	L	W	1113
GGG	TCA	GGG	CCC	ATC	TGG	CTG	GAT	GAC	CTG	AAC	TGC	ACA	GGA	ACG	GAG	TCC	CAC	TTG	TGG	3366
Q	C	P	S	R	G	W	G	Q	H	D	C	R	H	K	E	D	A	G	V	1133
CAG	TGC	CCT	TCC	CGC	GGC	TGG	GGG	CAG	CAC	CAC	TGC	AGG	CAC	AAG	GAG	GAC	GCA	GGG	GTC	3426
I	C	S	E	F	T	A	L	R	L	Y	S	E	T	E	T	E	S	C	A	1153
ATC	TGC	TCA	GAA	TTC	ACA	GCC	TTG	AGG	CTC	TAC	AGT	GAA	ACT	GAA	ACA	GAG	AGC	TGT	GCT	3486
G	R	L	E	V	F	Y	N	G	T	W	G	S	V	G	R	R	N	I	T	1173
GGG	AGA	TTG	GAA	GTC	TTC	TAT	AAC	GGG	ACC	TGG	GGC	AGC	GTC	GGC	AGG	AGG	AAC	ATC	ACC	3546
T	A	I	A	G	I	V	C	R	Q	L	G	C	G	E	N	G	V	V	S	1193
ACA	GCC	ATA	GCA	GGC	ATT	GTG	TGC	AGG	CAG	CAG	CTG	GGC	TGT	GGG	GAG	AAT	GGA	GTT	GTC	3606
L	A	P	L	S	K	T	G	S	G	F	M	W	V	D	D	I	Q	C	P	1213
CTC	GCC	CCT	TTA	TCT	AAG	ACA	GGC	TCT	GGT	TTC	ATG	TGG	GTG	GAT	GAC	ATT	CAG	TGT	CCT	3666
K	T	H	I	S	I	W	Q	C	L	S	A	P	W	E	R	R	I	S	S	1233
AAA	ACG	CAT	ATC	TCC	ATA	TGG	CAG	TGC	CTG	TCT	GCC	CCA	TGG	GAG	CGA	AGA	ATC	TCC	AGC	3726

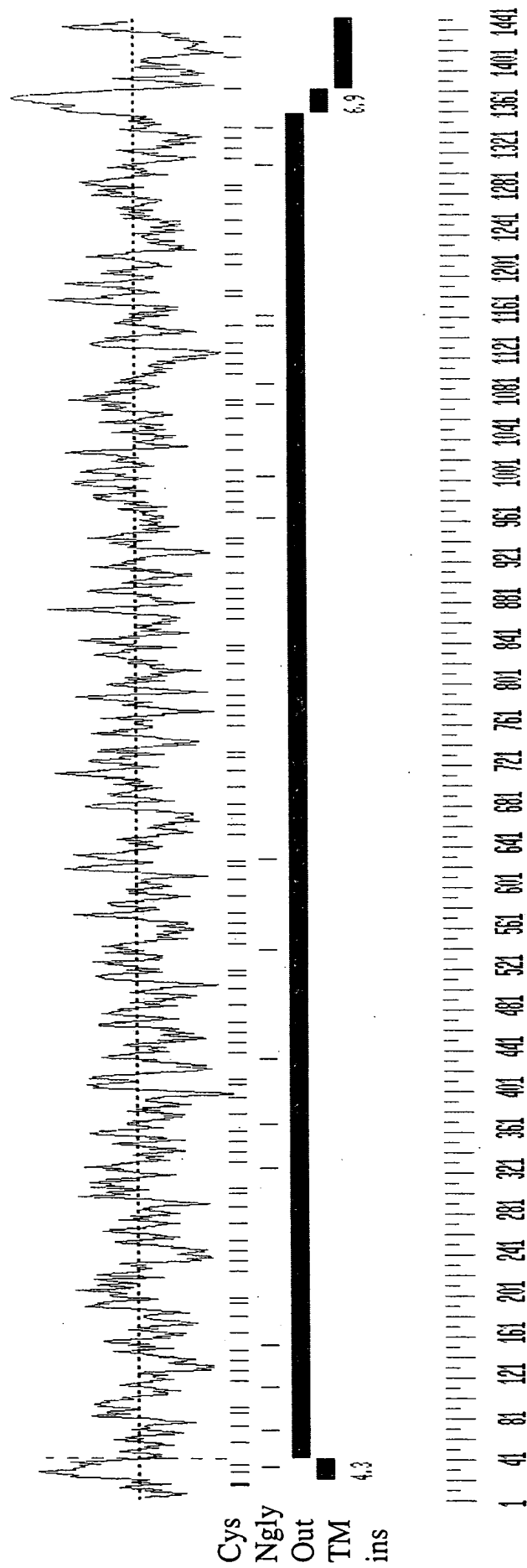
**Fig. 26G**

P	A	E	E	T	W	I	T	C	E	D	R	I	R	V	R	G	G	D	T	1253
CCA	GCA	GAA	GAG	ACC	TGG	ATC	ACA	TGT	GAA	GAT	AGA	ATA	AGA	GTG	CGT	GGA	GGA	GAC	ACC	3786
E	C	S	G	R	V	E	I	W	H	A	G	S	W	G	T	V	C	D	D	1273
GAG	TGC	TCT	GGG	AGA	GTG	GAG	ATC	TGG	CAC	GCA	GGC	TCC	TGG	GGC	ACA	GTG	TGT	GAT	GAC	3846
S	W	D	L	A	E	A	E	V	V	C	Q	Q	L	G	C	G	S	A	L	1293
TCC	TGG	GAC	CTG	GCC	GAG	GCG	GAA	GTG	GTG	TGT	CAG	CAG	CTG	GGC	TGT	GGC	TCT	GCT	CTG	3906
A	A	L	R	D	A	S	F	G	Q	G	T	G	T	I	W	L	D	D	M	1313
GCT	GCC	CTG	AGG	GAC	GCT	TCG	TTT	GGC	CAG	GGA	ACT	GGA	ACC	ATC	TGG	TTG	GAT	GAC	ATG	3966
R	C	K	G	N	E	S	F	L	W	D	C	H	A	K	P	W	G	Q	S	1333
CGG	TGC	AAA	GGA	AAT	GAG	TCA	TTT	CTA	TGG	GAC	TGT	CAC	GCC	AAA	CCC	TGG	GGA	CAG	AGT	4026
D	C	G	H	K	E	D	A	G	V	R	C	S	G	Q	S	L	K	S	L	1353
GAC	TGT	GGA	CAC	AAG	GAA	GAT	GCT	GGC	GTG	AGG	TGC	TCT	GGA	CAG	TCG	CTG	AAA	TCA	CTG	4086
N	A	S	S	G	H	L	A	L	I	L	S	S	I	F	G	L	L	L	L	1373
AAT	GCC	TCC	TCA	GGT	CAT	TTA	GCA	CTT	ATT	TTA	TCC	AGT	ATC	TTT	GGG	CTC	CTT	CTC	CTG	4146
V	L	F	I	L	F	L	T	W	C	R	V	Q	K	Q	K	H	L	P	L	1393
GTT	CTG	TTT	ATT	CTA	TTT	CTC	ACG	TGG	TGC	CGA	GTT	CAG	AAA	CAA	AAA	CAT	CTG	CCC	CTC	4206
R	V	S	T	R	R	R	G	S	L	E	E	N	L	F	H	E	M	E	T	1413
AGA	GTT	TCA	ACC	AGA	AGG	AGG	GGT	TCT	CTC	GAG	GAG	AAT	TTA	TTC	CAT	GAG	ATG	GAG	ACC	4266

**Fig. 26H**

C	L	K	R	E	D	P	H	G	T	R	T	S	D	D	T	P	N	H	G	1433
TGC	CTC	AAG	AGA	GAG	GAC	CCA	CAT	GGG	ACA	AGA	ACC	TCA	GAT	GAC	ACC	CCC	AAC	CAT	GGT	4326
C	E	D	A	S	D	T	S	L	L	G	V	L	P	A	S	E	A	T	K	1453
TGT	GAA	GAT	GCT	AGC	GAC	ACA	TCG	CTG	TTG	GGA	GTT	CTT	CCT	GCC	TCT	GAA	GCC	ACA	AAA	4386
*																				
TGA																				
1454																				
4389																				
C	T	T	T	A	G	A	C	T	T	C	A	G	G	C	T	C	A	A	C	4468
A	G	T	C	A	A	G	T	T	G	C	C	C	T	A	T	G	C	C	A	4547
T	G	A	T	A	A	A	A	T	T	A	A	A	A	A	A	A	A	A	A	4626
A	C																		4628	

Fig. 26I



**Fig. 26J**

	10	20	30	40	50	60	70	
Hum.	MMLPQNSWHIDFGRCCCHQNLFSAVVTCILLNSCFLISSFNQTDLELRLVNGDGPCSGTVEVKFQGWG							
	:	:	:	:	:	:	:	
	:	:	:	:	:	:	:	
WC1	MAL-----GR---HLSLRGL---CVLLLLGT--MVG---GQALELRLKDVHRCRCEGRVEVKHQGEWG	10	20	30	40	50		
	80	90	100	110	120	130		
Hum.	TVCDGWNNTASTVVCKQLGCPFSFAMFRFGQAVTR-HGKIWLDDVSCYGNESALWECQH--REWGSHN							
	:	:	:	:	:	:	:	
	:	:	:	:	:	:	:	
WC1	TVDGYRWTLKDASVVCRLGCGAAIG-FPGGAYFGPGLGPIWLLYTSCEGTESTVSDCEHSNIKDYRNDG	60	70	80	90	100	110	
	140	150	160	170	180	190	200	
Hum.	CYHGEDVGVCYGEANLGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLTAAVVCRLGCPSSFSSG							
	:	:	:	:	:	:	:	
	:	:	:	:	:	:	:	
WC1	YNHGRDAGVVCSG----FVRLAGGDGPCSGRVEVHSGEAWIPVSDGNFTLATAQIICAELGCGKAVSVLG	120	130	140	150	160	170	180
	210	220	230	240	250	260	270	
Hum.	VNSPAVLRPIWLDDILCQGNELALWNCRHRGWGNHDCSHNEDVTLTICYDSSDLELRLVGGTNRCMGRVE							
	:	:	:	:	:	:	:	
	:	:	:	:	:	:	:	
WC1	HELFRESSAQVWAEFRCEGEPELWVCPRPVCPGGTCHHSGSAQVVC SAYSEVRL-MTNGSSQCEGQVE	190	200	210	220	230	240	250

**Fig. 26K**

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      280      290      300      310      320      330      340
Hum. LKIQGRWGTVCHHKWNNAADVCKQLGCGTALHFAGLPHLQSGSDVVWLDGVSCSGNESFLWDCRHS GT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1 MNISQWRALCASHWSLANANVICRQLGCGVAISTPGPHLVEEGDQILTARFHCSGAESFLWSCPV TAL
      260      270      280      290      300      310      320

      350      360      370      380      390      400      410
Hum. VNFDC LHQNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNQALVVC KQLGCPFSV
      . :: : : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1 GGPDCSHGNTASVICS-GNQI-----QVLPQCND-----SV
      330      340      350

      420      430      440      450      460      470      480
Hum. FGSRRAKPSNEARDIWINNISCTGNESALWDCTYDGKAKRTCRRSDAGVICSDKADLDRLVGAHSPCY
      :: :: : : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1 -----SQPTGSA-----ASEDSA----PY-----CSDSRQL--RLVDGGGP CA
      360      370      380

      490      500      510      520      530      540      550
Hum. GRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
WC1 GRVEILDQGSWGTICDDGWDLD DARVVC RQLGCGEALNATGSAHFGAGSGPIWLDNLNCTGKESHVWRCP
      390      400      410      420      430      440      450

```

**Fig. 26L**



	560	570	580	590	600	610	620	
Hum.	HSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCGRLEVFYFQGRWGTVCDDGWNKAAA VVCSQLDC							
	460	470	480	490	500	510	520	
WC1	SRGWQHNCRHKQDAGVICS--EFLALRMVSEDQQCAGWLEVFYNGTWGVCVRNPMEDITVSTICRQLGC							
	630	640	650	660	670	680	690	
Hum.	PSSIIGMGLGNASTGYGKIWLDDVSCDGEDSLWSCRNSGWNDCSHSEDVGVICSDASDMELRLVGG							
	530	540	550	560	570	580	590	
WC1	GDSGTLNSSVALREGFRPQWVDRIQCRKTDTSLWQCPSPDPWNYNSCSPKEEAYIWCADSR--QIRLVDGG							
	700	710	720	730	740	750	760	
Hum.	SRCAGKVEVNVQGA VGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASL							
	600	610	620	630	640	650	660	
WC1	GRCSGRVEILDQGSWGTICDDRWDLDDARVVCKQLGCGEALDATVSSFFGTGSGPIWLDEVNCRGEESQV							
	770	780	790	800	810	820	830	
Hum.	WDCIRWEWKQTACHLNMEASLICS AHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCREL							
	670	680	690	700	710	720	730	
WC1	WRCPSWGWRQHNCNHQEDAGVICS GF--VRLAGGDGPCSGRVEVHSGEAWTPVSDGNFTLPTAQVICAEL							

**Fig. 26M**

	840	850	860	870	880	890	900
Hum.	NCGDAISLSVGDHFGKGNGLTWAЕКFQCEGSETHLALCPIVQHPEDTCIHSREVGVCSTRYTDVRLV-NG						
	:: ::::	:	:: ::::	:	:: ::::	:: ::::	:: ::::
WC1	GCGKAVSVLGHMPFRES	DGQVWAEFRCDGGEPELWSCPRVPCPGGTCLHSGAAQVVC	SVYTEVQLMKNG				
	740	750	760	770	780	790	800
	910	920	930	940	950	960	970
Hum.	KSQCDGQVEINVLGHWGSLCDTHWDPEDARVLCRQLSCGTALSTTGKYGIGERSVRVWGHFRHCLGNESL						
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
WC1	TSQCEGQVEMKISGRWRALCASHWSLANANVVC	RQLGCGVAISTPRGPHLVEGGDQISTAQFHCSGAESF					
	810	820	830	840	850	860	870
	980	990	1000	1010	1020	1030	1040
Hum.	LDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEG						
	:	:: ::::	:: ::::	:	:: ::::	:	:: ::::
WC1	LWSCPVTALGGPDCSHGNTASVICSGNHTQVLPQCNDFLSQPAGSAA	SESSPYCSDSRQLRLVDGGGPC					
	880	890	900	910	920	930	940
	1050	1060	1070	1080	1090	1100	1110
Hum.	AGRVEIYHDFWGTICDDGWDLSDAHVVCQKLGCGVAFNATVSAHFGE						
	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::	:: ::::
WC1	GGRVEILDQGSWGTICDDDDWDLD	DARVVC	RQLGCGEALNATGSAHF	GAGSGPIWLDD	DLNCTKESHVWRC		
	950	960	970	980	990	1000	1010

**Fig. 26N**

	1120	1130	1140	1150	1160	1170	1180
Hum.	PSRGWQHDCRHKEDAGVICSEFTALRLYSETETESCAGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLG						
	::::::::::	:::: ::	:::: ::	::::::::::	:::: ::	:::: ::	:::: ::
WC1	PSRGWRHDCRHKEDAGVICSEFLALRMVSEDQQ--CAGWLEVFYNGTWGSVCRSPMEDITVSVICRQLG						
	1020	1030	1040	1050	1060	1070	
	1190	1200	1210	1220	1230	1240	
Hum.	CGENGVS LAPLSKTGSGFMWVDDIQCPKTHISIWQCLAPWERRISSPAEETWITCEDR-----						
	::::: . . . ::	:::: ::	:::: ::	:::: ::	:::: ::	:::: ::	
WC1	CGDSGSLNTSVGLREGSRPRWVDLIQCRKMDTSLWQCPSPGWKYSSCSPKEEAYISCEGRRPKSCPTAAA						
	1080	1090	1100	1110	1120	1130	1140
	1250	1260	1270	1280	1290	1300	
Hum.	-----IRVRGGDTECSGRVEIWHAGSWGTVCDSDWDLAEAEVVCQQLGCGSALALRDASFQGGTGTIW						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	
WC1	CTDREKLRLRGGDSECSGRVEVWHNGSWGTVCDSDWSLAEAEVVCQQLGCGQALEAVRSAAFGPGNGSIW						
	1150	1160	1170	1180	1190	1200	1210
	1310	1320	1330	1340	1350	1360	
Hum.	LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSG-----QSLKSLNASSGHLALI						
	::::: : :: ::	:::: ::	:::: ::	:::: ::	:::: ::	:::: ::	
WC1	LDEVQCGGRESSLWDCVAEPWGQSDCKHEEDAGVRCSGVRTTLPTTAGTRTTSNSLPGIFSLPGVLC LI						
	1220	1230	1240	1250	1260	1270	1280

Fig. 260

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1370      1380      1390      1400      1410
Hum. LSSIFGLLLVLFLTWCRVQK-----QKHLPLRVS-----TRRRG-----SLEENLFHEME
      :.:.. :.:..: . .: : :... . . : . . : . . : . . : . . : . . :
WC1 LGSLFLVLVLVTQLLRW-RAERRALSSYEDALAEAVVEELDYLTTQKEGLGSPDQM TDVPDENYDDAE
1290      1300      1310      1320      1330      1340      1350

Hum. TC-----LKREDPHGTRTSD-----DTPNHGCEDAS-----DTSLLGVL
      . : .: :.:.:.. . .: : : . .: : . .: : . .: : . .: : . .: : . .: : . .: :
WC1 EVPVPGTPSPSQGNEEEVPEKEDGVRSSQTGSFLNFSREANPGEGEESFWLLQGKKGDAGYDDVELSA
1360      1370      1380      1390      1400      1410      1420

      1450
Hum. LPASEAT-K
      : .: .:
WC1 LGTSPVTFPS
1430
```

**Fig. 26P**

Hum.	ATGATGCTGCCCTCAA	AAC	T	CGTGG	CATAT	TGGA	AGATG	CTGCT	GCATC	AGAAC	CTTT	TCTCT	CTG
	:::		:::	:::		:::	:::		:::		:::		:::
WC1	ATG	-----G	CTC	TGG	-----	-----GC	AGACA	-----	-----C	CTCT	-----	CCCTG	-----
				10								20	
Hum.	CTGTGGTAACTTGC	ATCCCTG	CTCCCTG	AATTC	CTGCTT	TCTCAT	CAGCAG	TTTAA	TGGAAC	AGATT	TGGA		
	:	:	:	:	:	:	:	:	:	:	:	:	:
WC1	C-GGGGACTCT-G	TGTCCTC	CTCCT	-----	CGCA	-----	C-----	CATG	TGGTG	TGTC	AAAGCT	CTGGA	
	30	40	50					60	70	80			
Hum.	GTTGAGCTGGTCA	ATGGAGAC	GGTCCCTG	CTGCTG	GCACAG	TGGAGG	TGAAAT	CCAGG	GACAG	TGGGGG			
	:	:	:	:	:	:	:	:	:	:	:	:	:
WC1	GCTGAGGTTGA	AGGATGG	AGTCCAT	CGCTGT	GAGGGG	AGAGTG	GGAAG	TGAAG	CACCA	AGGAGA	TGGGGC		
	90	100	110	120	130	140	150						
Hum.	ACTGTGTGATG	ATGGGTG	GAACACT	ACTG	CCCT-CA	ACTG	TCGTG	CAAA	CAGCTT	GGATG	TCCAT	TTT	
	:	:	:	:	:	:	:	:	:	:	:	:	:
WC1	ACAGTGGATG	GTACAGG	TGGA-C	ATTGA	AGGATG	CATCTG	TAGTGT	GCAGAC	AGCTGGG	TGTGG	AGCT		
	160	170	180	190	200	210							

**Fig. 26Q-1**

```

280      290      300      310      320      330      340
Hum.  TCCTTCGCCAATGTTTCGTTTGGACAAGCCGTGA--CTAGACATGGAAAAAATTTGGCTTGATGATGTTTC
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   GCCATTG--GTTTCCCTGGAGGGGCTTATTTGGGCCAGGACTTGGCCCCCATTTGGCTTTTGATATACTTC
220    230    240    250    260    270    280
      350    360    370    380    390    400    410
Hum.  CTGTTATGGAAATGAGTCAGCTCTCTGGGAATGTCAACACCCGGAATGGGGAAGCCATAACTGTTATCAT
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   ATGTGAAGGGACAGAGTCAACTGTCACTGAGTCACTGTGAGCAT-TCTAATATTAAGAC-TATC-GTAATGAT
290    300    310    320    330    340    350
      420    430    440    450    460    470    480
Hum.  GGAGAAGATGTTGGTGTGAACGTGTATGGTGAAGCCAA-TCTGGGTTTGAG--GCTAG-TGGATGGAAAC
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   GGCATAATCATGATGTCGGGA--TGCTGGAGTAGTCTGCTCAGGATTTGTGCGTCTGGCTGGAGGGGATG
360    370    380    390    400    410    420
      490    500    510    520    530    540    550
Hum.  AACTCCTGTTCAGGGAGAGTGGAGGTGAAATTCCAAGAAAGGTGGGGGACTATATGTGATGATGGGTGGA
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
WC1   GAC-CCTGCTCAGGGCGAGTAGAAGTGCAATT--CTGGAGAAGCTTGGATCCCAGTGT-CTGATGGGAACT
430    440    450    460    470    480

```

**Fig. 26Q-2**

	560	570	580	590	600	610	620
Hum.	ACTTGAATACTGCTGCCGTGGTGTGCAGGCAACTAGGATGTCCATCTTCTTTTATTCTTCTGGAGTTGT						
	...	...	...	...	...	...	...
WC1	TCACACTTGCCACTGCC-----CAG-----ATCATCTGT-----GCAGAGTTGGG						
	490	500			510		520
	630	640	650	660	670	680	690
Hum.	TAATAGCCCTGCTGTATTGCGCCCCCATTTGGCTGGATGACATTTTATGCCAGGGAATGAGTTGGCACT-						
	...	...	...	...	...	...	...
WC1	TTGTGGC-----AAGGCTG--TGCTCTGT-----CCTGGGACATGAG----CTCTT						
	530		540		550		560
	700	710	720	730	740	750	760
Hum.	CTGGAATTGCAGACATCGTGGATGGGAAATCATGACTGCAGTCACAAATGAGGATGTCACATTAACTTGT						
	...	...	...	...	...	...	...
WC1	CAGAGAGTCCAGT-GCC-----CAGGTC TG--GGC---TGAAGAGTTCA-----GG						
	570	580		590		600	
	770	780	790	800	810	820	830
Hum.	TATGATAGTAGTGATCTTGAACTAAGGCTTGAGGTGGAAC TAACCGCTGTATGGGAGAGTAGAGCTGA						
	...	...	...	...	...	...	...
WC1	TGTGAGGGGAGGAGCCTGAGCT----CT-----GGGTCTGCCC-CAGAGTG-----CCCTG-						
	610	620	630		640		650

**Fig. 26Q-3**

	840	850	860	870	880	890	900
Hum.	AAATCCAAGGAAGTGGGGACCGTATGCCACCATAAGTGGAAACAATGCTGCAGCTGATGTCGTATGCAA						
	:::	:::	:::	:::	:::	:::	:::
WC1	-----TCCA-----GGGGCACGTGT--CACCACA-GTGGATC--TGCT-CAGGTTGTTTGTTCAGCAT						
	660	670	680	690	700		
	910	920	930	940	950	960	970
Hum.	GCAGTTGGGATGTGGAACCGCACCTTCACTTCGCTGGCTTGCCCTCATTTGCAGTCAGGGTCTGATGTTGTA						
	..	.....	.....	.....	.....	.....	.....
WC1	ACT-----CAGAACTCCGGCTCATGACAA-AC-GGCT--CCTC-TCAG-TGTGAAGGCGCAGGTGGAGAT						
	710	720	730	740	750	760	
	980	990	1000	1010	1020	1030	1040
Hum.	TGGCTTGATGGTGTCCTCGTCCGGTAATGAATCTTTCTTTGGACTGCAGACATTCCGGAACCGTCA						
	.....	...	.....	...	...	.....	:
WC1	GAACATT-----TCTG-GACAAATGGAGAGCGCTCTGTGCCCTCCC-CTGGAGTCTGGCCCAATGCC---A						
	770	780	790	800	810	820	
	1050	1060	1070	1080	1090	1100	1110
Hum.	ATTTTGACTGTCTTCATCAAAAACGATGTGTCTGTGATCTGCTCAGATGGAGCAGATTTGGAAC TCGGACT						
	::	.....	...	...	...	...	...
WC1	ATGTTATCTGTCGTAGCTCGGCTGTGGAGTTGCCATCTCCACCCCGGAG-----GACCAC-ACT						
	830	840	850	860	870	880	

**Fig. 26Q-4**



Hum.	1120	1130	1140	1150	1160	1170	1180
	AGCAGATGGAAGTAACAAT	TGTT	CAGGGAGAGTAGAGGT	GAGAA	TTCA-TGAACAGTGGTGGACAATATG		
WC1	TG---GTGGAAGAAG---	GTGATCAG--ATCCTAACAGCCCGATT	CACTGCTCTG----	GGGC----	TG		
	890	900	910	920	930		
Hum.	1190	1200	1210	1220	1230	1240	1250
	TGACCAGAACTGGAAGAA	TGAACAAGCCCTTG	TGGTTTGTAAAGCAGCTAGGATG	TCCGTT	CAGCGTCTTT		
WC1	AGTCCT-TCC	TGTGGAGTTGT-----CCT-GTGACT-----GCC-CTGGGTGGTCCCTGACTGTTCCCAT					
	940	950	960	970	980	990	
Hum.	1260	1270	1280	1290	1300	1310	1320
	GGCAG-TCGTCGTGCTAAACCTAGTAATGAAGCTAGAGACATTTGGATAAACAGCATATCTTGCAC	TGGG					
WC1	GGCAACACAGCCCTCTGTGATCTGCTCAGGAAACCAGATCCAGGTGCTTCCCCCAGTGCAACGA-CTCCG--						
	1000	1010	1020	1030	1040	1050	1060
Hum.	1330	1340	1350	1360	1370	1380	1390
	AATGAGTCAGCTCTCTGGGACTGCACATATGATGGAAAAGCAAGCAACATGCTTCCGAAAGATCAGATG						
WC1	--TGTCCTCAACCTACAGGCTCTGC-----GGC-----CTCAGAGGACA-GCGCCC-----CCTACTG						
	1070	1080	1090	1100			

**Fig. 26Q-5**

	1400	1410	1420	1430	1440	1450	1460
Hum.	CTGGAGTAATT	TGTTCTGATAA	AGGCAGATCT	GGACCTAAG	GCTTGT	CGGGCTCAT	AGCCCCCTGTTATGG
	::	::	::	::	::	::	::
	::	::	::	::	::	::	::
WC1	CTCAGA-----	CAG--CAGGCAGCT	CCG--CCTGGTG---	GACGGGG-GC--	GGTCCCTGCGCCGG		
1110		1120	1130		1140	1150	1160
	1470	1480	1490	1500	1510	1520	
Hum.	GAGATTGGAGGT	GAAATACCAAG	GAGAGTGGGGG	ACTGTGTGTCAT	GACAGATGG	GAGCACAAGG-AA	TGC
	::	::	::	::	::	::	::
	::	::	::	::	::	::	::
WC1	GAGAGTGGAGAT	CCCTTGACCA	GGGCTCCTGGGC	ACCATCTGTGAT	GACGGCTGGGAC-	CTGGACGATGC	
1170	1180	1190	1200	1210	1220		
	1530	1540	1550	1560	1570	1580	1590
Hum.	A-GCTGTTGTGT	GTAAACAATT	GGGATGTGGA-A	AGCCTATGCAT	GTGTTTGGTAT	GACCTATTTTAAAG	
	::	::	::	::	::	::	::
	::	::	::	::	::	::	::
WC1	CCGC-GTGGTGT	GCAGGCAGCT	GGGCTGTGGAG	AAGCCCTCA-ATGCC	ACGGGTCTGCT	CACCTTCGGGG	
1230	1240	1250	1260	1270	1280	1290	
	1600	1610	1620	1630	1640	1650	1660
Hum.	AAGCATCAGGAC	CTATT	TGGCTGGATGAC	GTTTCTTGCA	TGGAAATGAGT	CAAATATCTGGGACTGTGA	
	::	::	::	::	::	::	::
	::	::	::	::	::	::	::
WC1	CAGGATCAGGG	CCCCATCT	GTGGTGGACA	CACTTGA	ACTGCACAGG	AAAGGAGTCCCACGTGTGGAGGTGCC	
1300	1310	1320	1330	1340	1350	1360	

**Fig. 26Q-6**



	1950	1960	1970	1980	1990	2000	2010
Hum.	ATGTTTCCTGTGATGGAGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGTG--GGGAAATAATGAC						
	.....	.....	.....	.....	.....	.....	.....
WC1	-AGAAATCCAGTGTCTCGGAAACTGACACCTCTCT--CTGGCAGTGTCCCTTCTGACCCCTTGGAATTACAAC						
	1640	1650	1660	1670	1680	1690	1700
	2020	2030	2040	2050	2060	2070	2080
Hum.	TGCAGTCACAGTGAAGATGTTGGAGTG-ATCTGTTCTGATG-CATCGGATATGGAGCTGAGGCTTGTGGG						
	: : : : .	.....	.....	.....	.....	.....	.....
WC1	T-CATGCTCTCCAAAGGAGGAAGCCCTATATCTGGTGTGCAGACAGCAGACA--GATCCGC--CTGGTGGA						
	1710	1720	1730	1740	1750	1760	
	2090	2100	2110	2120	2130	2140	2150
Hum.	TGGAAGCAGCAGGTGTGCTGGAAAGTTGAGGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAAT						
	.....	.....	.....	.....	.....	.....	.....
WC1	TGGAGGTGGTCGCTGCTCTGGGAGAGTGGAGATCCTTGACCAGGGCTCCTGGGGCACCATCTGTGATGAC						
	1770	1780	1790	1800	1810	1820	1830
	2160	2170	2180	2190	2200	2210	2220
Hum.	GGCTGGGGAATGAACATTGCTGAAGTTGTTTGCAGGCAACTTGAATGTGGGTCTGCAATCAGGGTCTCCA						
	.....	.....	.....	.....	.....	.....	.....
WC1	CGCTGGGACCTGGACCGATCCCCGTGTGGTGTGCAAGCAGCTGGGCTGTGGAGAAGC---CCTGGACGCCA						
	1840	1850	1860	1870	1880	1890	1900

**Fig. 26Q-8**

	2230	2240	2250	2260	2270	2280
Hum.	GAGA-GCCTCATTTTCACAGAA--AGAACATTACACATCTTAATGTCGAATTC					
	1910	1920	1930	1940	1950	1960
WC1	CTGTCTCTTCCCTTCTTCGGACGGGATCAGGGCCCATCTGGCTGGATGAAGTGA					
	2290	2300	2310	2320	2330	2340
Hum.	AGCCTCTCTCTGGGATTGTATACGATGGGAGTGGAACAG-ACTGCCGTGTCA					
	1980	1990	2000	2010	2020	2030
WC1	GTCCCAAGTATGGAGGTGCCCTTCCTGGGATGGCGCAACACAAAC-TGCAATCATCAAGAA					
	2360	2370	2380	2390	2400	2410
Hum.	TTTGATCTGCTCAGCCACAGGCAGCCAGCGTGGTTGGAGCTGATATGCCCTGCTCTGGACGTGTGAA					
	2050	2060	2070	2080	2090	2100
WC1	AGTCATCTGCTCAGGATTGTGC-----GTCTGGCTGGAGGAGATGGACCCCTGCTCAGGGCGAGTAGAA					
	2430	2440	2450	2460	2470	2480
Hum.	GTGAAACATGCAGACACATAGCGCTCTGTCTGTGATTCTGATTCTCTCTTCA					
	2110	2120	2130	2140	2150	2160
WC1	GTGCATTCTGGAGAGCCCTGGACCCAGTGTCTGATGGAAACTTCACACTCCCCACTGCC					

Fig. 26Q-9

	2500	2510	2520	2530	2540	2550	2560
Hum.	GTGCAGAGAA	TTAAATTGTGGAGATGCCATATCTCTTTCTGTGGGAGATCACTTTGGAAAAGGG-AATGG					
	.....	.....	.....	.....	.....	.....	.....
WC1	GTGCAGAGC--TGGGATGTGGCAAGGCTGTGTCT-GTCCCTGGGACACATGCCATTTCAGAGAGTCCGATGG						
	2180	2190	2200	2210	2220	2230	2240
	2570	2580	2590	2600	2610	2620	2630
Hum.	TCTAACTTGGGCCGAAAAGTTCCAGTGTGAAGGGAGTGAAACTCACCTTGCAATTATGCCCCCATTTGTTCAA						
	....	.....	.....	.....	.....	.....	.....
WC1	CCAGGTCTGGGCTGAAGAGTTCAGGTGTGATGGGGGGAGCCCTGAGCTCTGGTCCCTGCCCCAGAGTGCCC						
	2250	2260	2270	2280	2290	2300	2310
	2640	2650	2660	2670	2680	2690	2700
Hum.	CATCCGGAAGACACTTGTATCCACAGCAGAGAAAGTTGGAGTTGTCTGTCTCCCGATATACAGATGTCCGAC						
	.....	.....	.....	.....	.....	.....	.....
WC1	TGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTTGTCTGTTCAGTGTACACAGAAAGTCCAGC						
	2320	2330	2340	2350	2360	2370	2380
	2710	2720	2730	2740	2750	2760	2770
Hum.	TTGTGAATGGCAAATCC--CAGTGTGACGGGCAAGTGGAGATCAACGTGCT-TGGACACTGGGGCTCAC						
	.....	.....	.....	.....	.....	.....	.....
WC1	TTATGAAAAACGGCACCTCTCAATGTGAGGGGCAGGTGGAGAT-GAAGATCTCTGGACGATGGAGAGCGC						
	2390	2400	2410	2420	2430	2440	2450

**Fig. 26Q-10**

	2780	2790	2800	2810	2820	2830	2840
Hum.	TGTGTGACACCCACTGGGACCAGAAAGATGCCCGTGTTCATGCAGACAGCTCAGCTGTGGGACTGCTCT						
	:	:	:	:	:	:	:
WC1	TCTGTGCCCTCCCCTGGAGTCTGGCCAATGTTGTCTGTCTCAGCTCGGCTGTGGAGTCGCCCAT						
	2460	2470	2480	2490	2500	2510	2520
	2850	2860	2870	2880	2890	2900	2910
Hum.	CTCAACCACAGGAGGAATAATATTGGAGAAAGAAGTGTTTCGTGTGTGGGACACAGGTTTCATTGCTTA						
	:	:	:	:	:	:	:
WC1	CTCCACCCCCAGAGGACCACACTTGGTGTGAAGGAGGTGATCAGATCTCAACAGCCCCAATTTCACTGCTCA						
	2530	2540	2550	2560	2570	2580	2590
	2920	2930	2940	2950	2960	2970	2980
Hum.	GGGAATGAGTCACCTTCTGGATAACTGTCAAATGACAGTCTCTGGAGCACCTCCCTGTATCCATGGAAATA						
	:	:	:	:	:	:	:
WC1	GGGGCTGAGTCCTTCCCTGTGGAGTTGTCTCTGTGACTGCCCTTGGGTGGCCTGACTGTTCCCATGGCAACA						
	2600	2610	2620	2630	2640	2650	2660
	2990	3000	3010	3020	3030	3040	3050
Hum.	CTGTCTCTGTGATCTGCACAGGAAGCCTGACCCAGCCACTGTTTCCATGCCCTCGCAAATGTATCTGACCC						
	:	:	:	:	:	:	:
WC1	CAGCCCTCTGTGATCTGCTCAGGAAACCACACCCAGGTGCTGCCCCAGTGCAACGACTTCCCTGTCTCAACC						
	2670	2680	2690	2700	2710	2720	2730

**Fig. 26Q-11**

	3060	3070	3080	3090	3100	3110	3120
Hum.	ATATTGCTGCAGTTCCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCCTAGTGGAT						
	.	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.
WC1	TGCAGGCTCTCGGGCCTCAGAGGAGAGTTCTCCCTACTGCTCAGACAGCAGGCTCCGCCCTGGTGGAC						
	2740	2750	2760	2770	2780	2790	2800
	3130	3140	3150	3160	3170	3180	3190
Hum.	GGGACAGCCGCTGTGCCGGGAGAGTAGAGATCTATCACGACGGCTTCTGGGGCACCATCTGTGATGACG						
	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.
WC1	GGGGCGGTCCCTGCGGGGAGAGTGAGATCCTTGACCAGGGCTCCTGGGCACCATCTGTGATGATG						
	2810	2820	2830	2840	2850	2860	2870
	3200	3210	3220	3230	3240	3250	3260
Hum.	GCTGGACCTGAGCGATGCCACGTCGTGTGTCAAAAGCTGGGCTGTGGAGTGGCCCTTCAATGCCACGGT						
	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.
WC1	ACTGGACCTGGACGATGCCCGTGTGGTGTGCAGGCAGCTGGGCTGTGGAGAAAGCCCTCAATGCCACGGG						
	2880	2890	2900	2910	2920	2930	2940
	3270	3280	3290	3300	3310	3320	3330
Hum.	CTCTGCTCACTTTGGGAGGGGTCAGGGCCCATCTGGCTGGATGACCTGAACCTGCACAGGAACGGAGTCC						
	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.	:::::.
WC1	GTCTGCTCACTTCGGGGCAGGATCAGGGCCCATCTGGCTGGACGACCTGAACCTGCACAGGAACGGAGTCC						
	2950	2960	2970	2980	2990	3000	3010

**Fig. 26Q-12**



	3340	3350	3360	3370	3380	3390	3400
Hum.	CAC	TGTGGCAGTGC	CCCTCCC	GCGGCTGGGGCAGCACGACTGCAGGCACAAGGAGACGACGGGTCA			
	:::	:::	:::	:::	:::	:::	:::
	WC1	CACGTGTGGAGGTGCCCTTCCCCGGGGCTGGGGCGGCACGACTGCAGACACAAGGAGACGCCGGGGTCA					
	3020	3030	3040	3050	3060	3070	3080
	3410	3420	3430	3440	3450	3460	3470
Hum.	TCTGCTCAGAATTACAGCCTTGAGGCTCTACAGTGAAACTGAACACAGAGAGCTGTGCTGGAGATTGGA						
	:::	:::	:::	:::	:::	:::	:::
	WC1	TCTGCTCAGAGTTCCCTGGCCCCTCAGGAT---GGTGAG-CGAGGACCAGCAG-TGTGCTGGGTGGCTGGA					
	3090	3100	3110	3120	3130	3140	
	3480	3490	3500	3510	3520	3530	3540
Hum.	AGTCTTCTATAACGGGACCTGGGGCAGCGTCGGCAGGAGGAACATCACACAGCCATAGCAGGCATTGTG						
	:::	:::	:::	:::	:::	:::	:::
	WC1	GGTTTTCTACAACGGGACCTGGGGCAGTGTCTGCCGAGCCCCCATGGAAGATATCACTGTGTCCGTGATC					
	3150	3160	3170	3180	3190	3200	3210
	3550	3560	3570	3580	3590	3600	
Hum.	TGCAGGCAGCTGGGCTGTGGGGAGAAATGGAGTTGTACGCCCTGCCCCCTTTA--TCT-AAGACAGGCTCTG						
	:::	:::	:::	:::	:::	:::	:::
	WC1	TGCAGACAGCTTGATGTGGGGACAGTGGA--AGTCT-CAACACCTCTGTTGGTCTCAGGGAAGGTTCTTA					
	3220	3230	3240	3250	3260	3270	3280

**Fig. 26Q-13**



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3840      3850      3860      3870      3880      3890      3900
Hum.  GGAAGTGGTGTCTCAGCAGCTGGGCTGTGGCTCTGGCTGCCCTGAGGACGCTTCGTTGGCCAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   TGAGGTGGTGTCTCAGCAGCTGGGCTGTGGCCAGGCCCTGGAAGCCGTGCGGTCTGCAGCATTTGGCCCT
3570      3580      3590      3600      3610      3620      3630

3910      3920      3930      3940      3950      3960      3970
Hum.  GGAAC TGGAA CCA TCTGG TTGGATGACATGCGGTGCA AAGGAAATGAGTCATTTCTATGGGACTGTCACG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   GGAAATGGGAGCATCTGGCTGGACGAGGTGCAGTGC GGGGGCCGGAGTCCTCCCTGTGGGACTGTGTTG
3640      3650      3660      3670      3680      3690      3700

3980      3990      4000      4010      4020      4030      4040
Hum.  CCAAACCTGGGGACAGAGTGACTGTGGACACAAAGGAAGATGCTGGCGTGAGGTGCTCTGG--ACAGTC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   CGGAGCCCTGGGGCAGAGCGACTGCAAGCACGAGGAGGATGCTGGTGTGAGGTGCTCTGGTGTAAAGGAC
3710      3720      3730      3740      3750      3760      3770

4050      4060      4070      4080      4090
Hum.  G-----CTGAAATCACTGAATG--CCT-----CCTCAGGT-CATT---TAGCA-CTTATTTTATCCA
      : . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WC1   AACATTGCCCCACGACCACAGCAGGACCAGAACAACCTCAAATTCCTCCCTGGCACTCTCTCCCTGCCT
3780      3790      3800      3810      3820      3830      3840

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**Fig. 26Q-15**

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4100      4110      4120      4130      4140
Hum. G-----TATCTT-----TGGGCTC-CTTCTC---CTGGTTCT-----GTTTATTCATTTCTCA
      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :
WC1 GGGGTTCTCTGCCCTTATCCTGGGTCGCTTCTCTCCCTGGTCCCTCGTCATCCTGGTGACTCAGCTACTCA
3850      3860      3870      3880      3890      3900      3910

4150      4160      4170      4180
Hum. CGTGGTG--CCGAGTTTCAGAAACAAAACATCT-----GCCC---CT-----CAGAGTTT-----
      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :
WC1 GATGGAGACAGAGCGCAGAGCCCTTATCCAGCTATGAAGATGCTCTTGGTGAAGCTGTGTATGAGGAGCT
3920      3930      3940      3950      3960      3970      3980

4190      4200      4210      4220
Hum. -----CAAC-----CAGAAGGAGG---GTTCT-CTCG---AGGAGAAATTATTCATGA-----
      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :
WC1 CGATTACCTTCTGACACAGAGAAGGAGTCTGGGCAGCCCAGATCAGATGACTGATGTCCCTGATGAAAAT
3990      4000      4010      4020      4030      4040      4050

4230      4240      4250
Hum. ---GATGGAG-----ACCTG-----CCTC-----AAGAGAGAGGAC
      :      :      :      :      :      :      :      :      :      :      :
      :      :      :      :      :      :      :      :      :      :      :
WC1 TATGATGATGCTGAAGAAGTACCAGTGCCTGGAACTCCTTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC
4060      4070      4080      4090      4100      4110      4120

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**Fig. 26Q-16**

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4260      4270      4280      4290
Hum. CCACATGGGACAAAGAAC-----CTCAGA-TGACAC---CC-----CCAA-----
      :: :: :::: ::::: ::::: ::::: ::::: :::::
WC1  CCCAGAGAAAGGAGGACGGGTGAGGTCTCTCAGACAGGCTCTTCCCTGAACCTTCTCCAGAGAGGCAGC
4130      4140      4150      4160      4170      4180      4190

      4300      4310      4320      4330
Hum. ----CCATGGTT--GTGAAGA----TGCTAGCGACAC-----ATCGCTG--TTGGGAGTT
      :: :: . ::::: : ::::: ::::: .. :::: :. :::::
WC1  TAATCCCTGGGAAGGAGAGAGAGCTTCTGGCTGCTCCAGGGGAAGAGGGATGCTGGGTATGATGAT
4200      4210      4220      4230      4240      4250      4260

      4340      4350
Hum. CTT-----CCTG-----CCTCTGAAGCCACAAAA
      :: :::: ::::: ::::: ::::: :::::
WC1  GTTGAACTCAGTGCCCTGGGAACATCCCCAGTGACTTTCTCTCG
4270      4280      4290      4300

```

**Fig. 26Q-17**

GTCGACCCACGCGTCCGGTCTGTGGCTGAGC	M	A	L	P	A	L	G	L	D	P	W	S	12
	ATG	GCC	CTC	CCA	GCC	CTG	GGC	CTG	GAC	CCC	TGG	AGC	67
L L G L L F L Q L L L L L P T T A G													32
CTC CTG GGC CTT TTC CTC TTC CAA CTG CTT CAG CTG CTG CTG CCG ACG ACG ACC GCG GGG													127
G G G Q G P M P R V R Y Y A G D E R A													52
GGA GGC GGC CAG GGC CCC ATG CCC AGG GTC AGA TAC TAT GCA GGG GAT GAA CGT AGG GCA													187
L S F F H Q K G L Q Q D F D T L L L S G D													72
CTT AGC TTC TTC CAC CAG AAG GGC CTC CAG GAT TTT GAC ACT CTG CTC CTG AGT GGT GAT													247
G N T L L Y V G A R E A I L A L D I Q D P													92
GGA AAT ACT CTC TAC GTG GGC GCT CGA GAA GCC ATT CTG GCC TTG GAT ATC CAG GAT CCA													307
G V P R L L K N M I P W P A S D R K K S E													112
GGG GTC CCC AGG CTA AAG AAC ATG ATA CCG TGG CCA GCC AGT GAC AGA AAA AAG AGT GAA													367
C A F K K K S N E T Q C F N F I R V L V													132
TGT GCC TTT AAG AAG AAG AGC AAT GAG ACA CAG TGT TTC AAC TTC ATC CGT GTC CTG GTT													427
S Y N V T H L Y T C G T F A F S P A C T													152
TCT TAC AAT GTC ACC CAT CTC TAC ACC TGC GGC ACC TTC GCC TTC AGC CCT GCT TGT ACC													487
F I E L L Q D S Y L L P I S E D K V M E G													172
TTC ATT GAA CTT CAA GAT TCC TAC CTG TTG CCC ATC TCG GAG GAC AAG GTC ATG GAG GGA													547

**Fig. 27A**

K	G	Q	S	P	F	D	P	A	H	K	H	T	A	V	L	V	D	G	M	192
AAA	GGC	CAA	AGC	CCC	TTT	GAC	CCC	GCT	CAC	AAG	CAT	ACG	GCT	GTC	TTG	GTG	GAT	GGG	ATG	607
L	Y	S	G	T	M	N	N	F	L	G	S	E	P	I	L	M	R	T	L	212
CTC	TAT	TCT	GGT	ACT	ATG	AAC	AAC	TTC	CTG	GGC	AGT	GAG	CCC	ATC	CTG	ATG	CGC	ACA	CTG	667
G	S	Q	P	V	L	K	T	D	N	F	L	R	W	L	H	H	D	A	S	232
GGA	TCC	CAG	CCT	GTC	CTC	AAG	ACC	GAC	AAC	TTC	CTC	CGC	TGG	CTG	CAT	CAT	GAC	GCC	TCC	727
F	V	A	A	I	P	S	T	Q	V	V	Y	F	F	F	E	E	T	A	S	252
TTT	GTG	GCA	GCC	ATC	CCT	TCG	ACC	CAG	GTC	GTC	TAC	TTC	TTC	TTC	GAG	GAG	ACA	GCC	AGC	787
E	F	D	F	F	E	R	L	H	T	S	R	V	A	R	V	C	K	N	D	272
GAG	TTT	GAC	TTC	TTT	GAG	AGG	CTC	CAC	ACA	TCG	CGG	GTG	GCT	AGA	GTC	TGC	AAG	AAT	GAC	847
V	G	G	E	K	L	L	Q	K	K	W	T	T	F	L	K	A	Q	L	L	292
GTG	GGC	GGC	GAA	AAG	CTG	CTG	CAG	AAG	AAG	TGG	ACC	ACC	TTC	CTG	AAG	GCC	CAG	CTG	CTC	907
C	T	Q	P	G	Q	L	P	F	N	V	I	R	H	A	V	L	L	P	A	312
TGC	ACC	CAG	CCG	GGG	CAG	CTG	CCC	TTC	AAC	GTC	ATC	CGC	CAC	GCG	GTC	CTG	CTC	CCC	GCC	967
D	S	P	T	A	P	H	I	Y	A	V	F	T	S	Q	W	Q	V	G	G	332
GAT	TCT	CCC	ACA	GCT	CCC	CAC	ATC	TAC	GCA	GTC	TTC	ACC	TCC	CAG	TGG	CAG	GTT	GGC	GGG	1027
T	R	S	S	A	V	C	A	F	S	L	L	D	I	E	R	V	F	K	G	352
ACC	AGG	AGC	TCT	GCG	GTT	TGT	GCC	TTC	TCT	CTC	TTG	GAC	ATT	GAA	CGT	GTC	TTT	AAG	GGG	1087

**Fig. 27B**

K	Y	K	E	L	N	K	E	T	S	R	W	T	T	Y	R	G	P	E	T	372
AAA	TAC	AAA	GAG	TTG	AAC	AAA	GAA	ACT	TCA	CGC	TGG	ACT	ACT	TAT	AGG	GGC	CCT	GAG	ACC	1147
N	P	R	P	G	S	C	S	V	G	P	S	S	D	K	A	L	T	F	M	392
AAC	CCC	CGG	CCA	GGC	AGT	TGC	TCA	GTG	GGC	CCC	TCC	TCT	GAT	AAG	GCC	CTG	ACC	TTC	ATG	1207
K	D	H	F	L	M	D	E	Q	V	V	G	T	P	L	L	V	K	S	G	412
AAG	GAC	CAT	TTC	CTG	ATG	GAT	GAG	CAA	GTG	GTG	GGG	ACG	CCC	CTG	CTG	GTG	AAA	TCT	GGC	1267
V	E	Y	T	R	L	A	V	E	T	A	Q	G	L	D	G	H	S	H	L	432
GTG	GAG	TAT	ACA	CGG	CTT	GCA	GTG	GAG	ACA	GCC	CAG	GGC	CTT	GAT	GGG	CAC	AGC	CAT	CTT	1327
V	M	Y	L	G	T	T	T	G	S	L	H	K	A	V	V	S	G	D	S	452
GTC	ATG	TAC	CTG	GGA	ACC	ACC	ACA	GGG	TCG	CTC	CAC	AAG	GCT	GTG	GTA	AGT	GGG	GAC	AGC	1387
S	A	H	L	V	E	E	I	Q	L	F	P	D	P	E	P	V	R	N	L	472
AGT	GCT	CAT	CTG	GTG	GAA	GAG	ATT	CAG	CTG	TTC	CCT	GAC	CCT	GAA	CCT	GTT	CGC	AAC	CTG	1447
Q	L	A	P	T	Q	G	A	V	F	V	G	F	S	G	G	V	W	R	V	492
CAG	CTG	GCC	CCC	ACC	CAG	GGT	GCA	GTG	TTT	GTA	GGC	TTC	TCA	GGA	GGT	GTC	TGG	AGG	GTG	1507
P	R	A	N	C	S	V	Y	E	S	C	V	D	C	V	L	A	R	D	P	512
CCC	CGA	GCC	AAC	TGT	AGT	GTC	TAT	GAG	AGC	TGT	GTG	GAC	TGT	GTC	CTT	GCC	CGG	GAC	CCC	1567
H	C	A	W	D	P	E	S	R	T	C	C	L	L	S	A	P	N	L	N	532
CAC	TGT	GCC	TGG	GAC	CCT	GAG	TCC	CGA	ACC	TGT	TGC	CTC	CTG	TCT	GCC	CCC	AAC	CTG	AAC	1627

**Fig. 27C**



S	W	K	Q	D	M	E	R	G	N	P	E	W	A	C	A	S	G	P	M	552
TCC	TGG	AAG	CAG	GAC	ATG	GAG	CGG	GGG	AAC	CCA	GAG	TGG	GCA	TGT	GCC	AGT	GGC	CCC	ATG	1687
S	R	S	L	R	P	Q	S	R	P	Q	I	I	K	E	V	L	A	V	P	572
AGC	AGG	AGC	CTT	CGG	CCT	CAG	AGC	CGC	CCG	CAA	ATC	ATT	AAA	GAA	GTC	CTG	GCT	GTC	CCC	1747
N	S	I	L	E	L	P	C	P	H	L	S	A	L	A	S	Y	Y	W	S	592
AAC	TCC	ATC	CTG	GAG	CTC	CCC	TGC	CCC	CAC	CTG	TCA	GCC	TTG	GCC	TCT	TAT	TAT	TGG	AGT	1807
H	G	P	A	A	V	P	E	A	S	S	T	V	Y	N	G	S	L	L	L	612
CAT	GGC	CCA	GCA	GCA	GTC	CCA	GAA	GCC	TCT	TCC	ACT	GTC	TAC	AAT	GGC	TCC	CTC	TTG	CTG	1867
I	V	Q	D	G	V	G	G	L	Y	Q	C	W	A	T	E	N	G	F	S	632
ATA	GTG	CAG	GAT	GGA	GTT	GGG	GGT	CTC	TAC	CAG	TGC	TGG	GCA	ACT	GAG	AAT	GGC	TTT	TCA	1927
Y	P	V	I	S	Y	W	V	D	S	Q	D	Q	T	L	A	L	D	P	E	652
TAC	CCT	GTG	ATC	TCC	TAC	TGG	GTG	GAC	AGC	CAG	GAC	CAG	ACC	CTG	GCC	CTG	GAT	CCT	GAA	1987
L	A	G	I	P	R	E	H	V	K	V	P	L	T	R	V	S	G	G	A	672
CTG	GCA	GGC	ATC	CCC	CGG	GAG	CAT	GTG	AAG	GTC	CCG	TTG	ACC	AGG	GTC	AGT	GGT	GGG	GCC	2047
A	L	A	A	Q	Q	S	Y	W	P	H	F	V	T	V	T	V	L	F	A	692
GCC	CTG	GCT	GCC	CAG	CAG	TCC	TAC	TGG	CCC	CAC	TTT	GTC	ACT	GTC	ACT	GTC	CTC	TTT	GCC	2107
L	V	L	S	G	A	L	I	I	L	V	A	S	P	L	R	A	L	R	A	712
TTA	GTG	CTT	TCA	GGA	GCC	CTC	ATC	ATC	CTC	GTG	GCC	TCC	CCA	TTG	AGA	GCA	CTC	CGG	GCT	2167

**Fig. 27D**

R	G	K	V	Q	G	C	E	T	L	R	P	G	E	K	A	P	L	S	R		732
CGG	GGC	AAG	GTT	CAG	GGC	TGT	GAG	ACC	CTG	CGC	CCT	GGG	GAG	AAG	GCC	CCG	TTA	AGC	AGA		2227
E	Q	H	L	Q	S	P	K	E	C	R	T	S	A	S	D	V	D	A	D		752
GAG	CAA	CAC	CTC	CAG	TCT	CCC	AAG	GAA	TGC	AGG	ACC	TCT	GCC	AGT	GAT	GTG	GAC	GCT	GAC		2287
N	N	C	L	G	T	E	V	A	*											762	
AAC	AAC	TGC	CTA	GGC	ACT	GAG	GTA	GCT	TAA											2317	
ACT	CTA	GGC	AC	AGG	CGG	CTG	CGG	TGC	AGG	CAC	CTG	GCC	CAT	GTG	CTG	GGC	GGC	CCCA	AGCAC	AGCCCTGACTAGGA	2396
TGAC	AGC	AGC	ACAA	AAG	AC	CTT	CTC	CCCTG	AGAG	AGCTT	CTG	CTACT	CTG	CACTG	CACTG	ATG	ATG	ACACT	CAGCAGGG	2475	
TGAT	GCAC	AGC	AGT	CTGCC	CTCCCT	TAT	GGG	ACT	CCCTT	CTAC	CAAG	CAC	ATG	AGCT	CTCT	TAAC	AGGT	GGGG	CTACCC	2554	
CCAG	ACCT	GTCT	CTAC	ACTG	ATATT	GAAGA	ACCT	GGAG	AGAT	CCCT	CAGT	TTCT	GGCC	ATTC	AGG	ACC	CTCC	AGAAA		2633	
CAC	AGT	TTCA	AGAG	ATCCT	AAAA	AACT	GCCT	GTCCC	AGG	ACCC	TAT	GGT	ATGA	ACAC	CCAA	CACT	TAACA	CAATC		2712	
ATAT	GCTA	ACAT	GCC	ACTC	CTGG	AACT	CCACT	CTGA	AGCT	GCCG	CTTT	GGAC	ACCA	CACT	CCCT	TCT	CCCC	AGGGTCA		2791	
TGC	AGG	ATCT	GTCC	CTCC	TGCT	TCCCT	TAC	CAGT	CGTG	CAC	CGCT	GACT	CCC	AGGA	GTCT	TTCT	GAA	GTCTGACC		2870	
ACCT	TTCT	TTCT	GTCT	TCAGT	TGGG	CAG	ACT	CTG	ATCC	CTT	CTGCC	CTGG	CAG	AATG	G	AGGG	TAAT	CTGAG	CCCTTCT	2949	
TCAC	TCCT	TTAC	CCCT	AGCT	GAC	CCCT	TCAC	CTC	CTCC	CTCC	CTTT	TCT	TTG	GGAT	TCAG	AAAA	AACT	GCTTGTC		3028	
AGAG	ACT	GTTT	ATTTT	TATT	AAAA	ATATA	AAGG	CTT	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AGGCGGCCGC		3104	

Fig. 27E



	290	300	310	320	330	340	350
Hum.	KKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	KKWTTFLKAQLLCAQPGQLPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF						
	290	300	310	320	330	340	350
	360	370	380	390	400	410	420
Hum.	KGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLLMDEQVVGTPLLVKSGVEYTRLAV						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	KGKYKELNKETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFLLMDEHVVGTPLLVKSGVEYTRLAV						
	360	370	380	390	400	410	420
	430	440	450	460	470	480	490
Hum.	ETAQGLDGHSHLVMLGTTTGLSHKAVVSGDSSAHLVEEIQLPDPEPVRNLQLAPTQGA VFGFSGGVW						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	ESARGLDGSSHVMYLGTSTGPLHKAVVPQDSSAYLVEEIQLPDSEPVRLQLAPAQGA VFAFGSGGIW						
	430	440	450	460	470	480	490
	500	510	520	530	540	550	560
Hum.	RVPRANC SVYESCVDCVLARDPHCAWD PESRTCCLLSAPNLNSWKQDMERGNPEWACASGPM SRS LRPQS						
	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
Mur.	RVPRANC SVYESCVDCVLARDPHCAWD PESRLCSLLSGST-KPWKQDMERGNPEWVCTRGP MARS PRRQS						
	500	510	520	530	540	550	

Fig. 27G

	570	580	590	600	610	620	630
Hum.	RPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG						
	.....	.....	.....	.....	.....	.....	.....
Mur.	PPQLIKEVLTVPNSILELRCPHLSALASYWWSHGGRAKISEASATVYNGSLLLIPQDGVGGLYQCVATENG						
	560	570	580	590	600	610	620
	640	650	660	670	680	690	700
Hum.	FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTLFALVLSGALI						
	.....	.....	.....	.....	.....	.....	.....
Mur.	YSYPVVSYWVDSQDQPLALDPELAGVPREVRVQVPLTRVGGASMAAQRSYWPHFLIVTVLLAIVLLGLT						
	630	640	650	660	670	680	690
	710	720	730	740	750	760	
Hum.	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA						
	.....	.....	.....	.....	.....	.....	.....
Mur.	LLLASPLGALRARGKVQCGMLPPREKAPLSRDQHLQPSKDHRTSASDVDADNNHLGAEVA						
	700	710	720	730	740	750	760

**Fig. 27H**

[illegible]

**Fig. 27I**

	250	260	270	280	290	300	310
Hum.	ATGGAATACTCTCTACGTGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGTCCC						
	::: :	::: :	::: :	::: :	::: :	::: :	::: :
Mur.	ATGGCAACACTCTCTATGTGGGGCTCGAGAGACCGTCCCTGGCCTTGAATATCCAGAACCCAGGAATCCC						
	280	290	300	310	320	330	340
	320	330	340	350	360	370	380
Hum.	CAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCCTTTAAGAAAG						
	::: :	::: :	::: :	::: :	::: :	::: :	::: :
Mur.	AAGGCTAAAGAACATGATACCCCTGGCCAGCCAGTGAGAGAAAAAGACCCGAATGTGCCCTTTAAGAAAG						
	350	360	370	380	390	400	410
	390	400	410	420	430	440	450
Hum.	AGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCT						
	::: :	::: :	::: :	::: :	::: :	::: :	::: :
Mur.	AGCAATGAGACACAGTGTTTCAACTTCATTCGAGTCCTGGTCTCTTACAATGCTACTCACCTCTATGCCT						
	420	430	440	450	460	470	480
	460	470	480	490	500	510	520
Hum.	GCGGCACCTTCGCCCTTCAGCCCCTGCTTGACCTTCATTGAACCTCAAGATTCCATCCTGTTGCCCATCTC						
	:	:	:	:	:	:	:
Mur.	GTGGGACCTTTGCCCTTCAGCCCCTGCCTGTACCTTCATTGAACCTCAAGATTCCCTCCTGTTGCCCATCTT						
	490	500	510	520	530	540	550

**Fig. 27J**

	530	540	550	560	570	580	590
Hum.	GGAGGACAAGGT	CATGGAGG	AAAGGCCAAAG	CCCCCTTTG	ACCCCGCTC	ACAAGCATACG	-GCTGTCTT
	.....	.....	.....	.....	.....	.....	.....
Mur.	GATAGACAAGGT	CATGGACGG	GAAGGCCAAAG	CCCC-TTTG	ACCCCTGTT	CACAAGCACACA	AGCTGTCTT
	560	570	580	590	600	610	620
	600	610	620	630	640	650	660
Hum.	GGTGGATGGG	ATGCTCTATT	CTGGTACTAT	GAACAACTT	CCTGGGCAGT	GAGCCCATC	CTGATGCGCACA
	::: ::	.....	.....	.....	.....	.....	.....
Mur.	GGTCGATGGG	ATGCTTTATT	CCGGCACCAT	GAACAACTT	CCTGGGCAG	GAGCCCATC	CTGATGCGGACA
	630	640	650	660	670	680	690
	670	680	690	700	710	720	730
Hum.	CTGGGATCCC	AGCCTGTCT	CAAGACCGACA	ACTTCTCCT	CGCTGGCTG	CATCATGAC	GCCTCTTGTGG
	.....	.....	.....	.....	.....	.....	.....
Mur.	CTGGGATCCC	ATCCTGTTCT	CAAGACTGACA	TCTTCTTAC	GTGGCTGCAC	GCGGATGC	CTCCTTCGTGG
	700	710	720	730	740	750	760
	740	750	760	770	780	790	800
Hum.	CAGCCATCCC	TCGACCCAGG	TCGTCTACTT	CTTCTTCG	AGGAGACAG	CCAGCGAGTT	TGACTTCTTTGA
	.....	.....	.....	.....	.....	.....	.....
Mur.	CAGCCATTCC	ATCCACCCAGG	TCGTCTATT	TCTTCTTTG	AGGAGACAG	CCAGCGAGTT	TGACTTCTTTGA
	770	780	790	800	810	820	830

**Fig. 27K**



	810	820	830	840	850	860	870
Hum.	GAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAAATGACGTGGCGGGCGGAAAAGCTGCTGCAGAAG						
	840	850	860	870	880	890	900
Mur.	AGAGCTGTATATATCCAGGGTGGCTCAAGTCTGCAAGAACGACGTGGCGGGTGAAGCTGCTGCAGAAG						
	880	890	900	910	920	930	940
Hum.	AAGTGGACCACCTTCCTGAAGCCCAGCTGCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCC						
	910	920	930	940	950	960	970
Mur.	AAGTGGACCACCTTCCTCAAAGCCCAGTTGCTCTGCGCTCAGCCAGGGCAGCTGCCATTCAACATCATCC						
	950	960	970	980	990	1000	1010
Hum.	GCCACGGGTCCTGCTCCCCCGCGGATTCTCCACAGCTCCCCACATCTACGCAGTCTTCACTCCAGTG						
	980	990	1000	1010	1020	1030	1040
Mur.	GCCACGGGTCCTGCTGCCCGCGGATTCTCCCTCTGTGTTCCCGCATCTACGCAGTCTTTACCTCCAGTG						
	1020	1030	1040	1050	1060	1070	1080
Hum.	GCAGGTTGGCGGACCAGGAGCTCTGCGGTTTGTGCCCTTCTCTCTTGGACATTGAACGTGCTTTAAG						
	1050	1060	1070	1080	1090	1100	1110
Mur.	GCAGGTTGGCGGACCAGGAGCTCAGCAGTCTGTGCCCTTCTCTCTCAGGACATTGAGCGAGTCTTTAA						

**Fig. 27L**

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1090      1100      1110      1120      1130      1140      1150
Hum.  GGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGGAGTACAAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACTTACCGGGGCTCAGAGGTCAGCCCCGA
1120      1130      1140      1150      1160      1170      1180

1160      1170      1180      1190      1200      1210      1220
Hum.  GGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGCCAGGCAGTTGCTCCATGGGCCCTCCTCTGACAAAGCCTTGACCTTCATGAAGGACCATTTCCTGAT
1190      1200      1210      1220      1230      1240      1250

1230      1240      1250      1260      1270      1280      1290
Hum.  GGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAAATCTGGCTGGAGTATACACGGCTTGCAGTGGAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  GGATGAGCACGTGGTAGGAACACCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTGGAG
1260      1270      1280      1290      1300      1310      1320

1300      1310      1320      1330      1340      1350      1360
Hum.  ACAGCCCAGGGCCTTGATGGGCACAGCCCATCTTGTCATGTACCTGGGAACCAACACAGGTCGCTCCACA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Mur.  TCAGCTCGGGGCCTTGATGGGAGCAGCCCATGTGGTCATGTATCTGGGTACCTCCACGGGTCCTCCCTGCACA
1330      1340      1350      1360      1370      1380      1390

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Fig. 27M

	1370	1380	1390	1400	1410	1420	1430
Hum.	AGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAGAGATTTCAGCTGTTCCCTGACCCCTGAACC						
	::::::::::::	:	::::::::::::	::::	::::::::::::	::::	::::::::::::
Mur.	AGGCTGTGGTGCCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATTTCAGCTGAGCCCTGACTCTGAGCC						
	1400	1410	1420	1430	1440	1450	1460
	1440	1450	1460	1470	1480	1490	1500
Hum.	TGTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAAGTGTTCGTAGGCTTCTCAGGAGGTGTCTGGAGG						
	:::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::
Mur.	TGTTCGAAACCTGCAGCTGGCCCCCGCCCCAGGGTGCAAGTGTTCGTAGGCTTCTCTGGAGGCATCTGGAGA						
	1470	1480	1490	1500	1510	1520	1530
	1510	1520	1530	1540	1550	1560	1570
Hum.	GTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTCCCTGCCCCGGACCCCACTGTG						
	::	::	::::::::::::	::::::::::::	::::::::::::	::::::::::::	::::::::::::
Mur.	GTTCCCAGGGCCAAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCCAGGGACCCCTCACTGTG						
	1540	1550	1560	1570	1580	1590	1600
	1580	1590	1600	1610	1620	1630	1640
Hum.	CCTGGGACCCCTGAGTCCCGAACCTGTTGCCCTCCTGTCTGCCCCCAACCTGAACCTCCTGGAAGCAGGACAT						
	::::::::::::	::::	::::	::::::::::::	:	::::	::::::::::::
Mur.	CCTGGGACCCCTGAATCAAGACTCTGCAGCCCTTCTGTCTGGCTC-TACCAAGCCT--TGGAAGCAGGACAT						
	1610	1620	1630	1640	1650	1660	1670

**Fig. 27N**

	1650	1660	1670	1680	1690	1700	1710
Hum.	GGAGCGGGGA	ACCCAGAGTGGGCATGTGCCAGTGGCCCCCATGAGCAGGAGCCCTTCGGCCCTCAGAGCCGC					
	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
Mur.	GGAACGCGGA	ACCCGGAGTGGGTATGCACCCGTGGCCCCCATGGCCAGGAGCCCCCGCGTCAAGAGCCCC					
	1680	1690	1700	1710	1720	1730	1740
	1720	1730	1740	1750	1760	1770	1780
Hum.	CCGCAATCAT	TAAAGAGTCCTGGCTGTCCCAACTCCATCCTGGAGCTCCCCCTGCCCCACCTGTCTAG					
	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
Mur.	CCTCAACTAA	TAAAGAGTCCTGACAGTCCCAACTCCATCCTGGAGCTGGCTGCCCCACCTGTCTAG					
	1750	1760	1770	1780	1790	1800	1810
	1790	1800	1810	1820	1830	1840	1850
Hum.	CCTTGGCCCT	TATTATTGGAGTCATGGCCAGCAGCAGTCCAGAGCCTCTTCCACTGTCTACAATGG					
	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
Mur.	CACTGGCCCT	TTACCACCTGGAGTCATGGCCGAGCCAAAATCTCAGAAAGCCTCTGTACCGTCTACAATGG					
	1820	1830	1840	1850	1860	1870	1880
	1860	1870	1880	1890	1900	1910	1920
Hum.	CTCCCTCTTG	CTGATAGTGCAGGATGGAGTTGGGGTCTCTACCAAGTGTGGCAACTGAGAAATGGCTTT					
	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
Mur.	CTCCCTCTTG	CTGCTGCCGAGGATGGTGTCTGGGGCCCTCTACCAGTGTGTGGCGACTGAGAACGGCTAC					
	1890	1900	1910	1920	1930	1940	1950

**Fig. 270**

	1930	1940	1950	1960	1970	1980	1990
Hum.	TCATACCCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCCTGGCCCTGGATCCTGAAC	TTGGCAG					
	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::	::::::::::::::::
Mur.	TCATACCCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCTGGCGCTGGACCCCTGAGCTGGCGG						
	1960	1970	1980	1990	2000	2010	2020
	2000	2010	2020	2030	2040	2050	2060
Hum.	GCATCCCCCGGAGCATGTGAAGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCA						
	::: ::::	::::::::	::::::::	::::::::	::::::::	:: ::::	::::::::
Mur.	GCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGCGGAGCTTCCATGGCTGCCCAGCG						
	2030	2040	2050	2060	2070	2080	2090
	2070	2080	2090	2100	2110	2120	2130
Hum.	GTCCCTACTGGCCCCACTTTGTCACTGTCACTGTCCCTCTTGGCCTTAGTGCTTTCAGGAGCCCTCATCATC						
	::::::::::::::::	:: ::	:::::	:::::	:::::	:::::	:: ::
Mur.	GTCCCTACTGGCCCCCATTTTCTCATCGTTACCGTCCCTCCCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTC						
	2100	2110	2120	2130	2140	2150	2160
	2140	2150	2160	2170	2180	2190	2200
Hum.	CTCGTGGCCCTCCCCATTGAGAGCACTCCGGGCTCGGGCAAGGTTCAAGGCTGTGAGACCCCTGCGCCCTG						
	::: : ::	:::::	:::::	:::::	:::::	:::::	::: :::
Mur.	CTCCTCGCTTCCCCACTGGGGGCGCTGCGGGCTCGGGGTAAGTTCAAGGCTGTGGGATGCTGCCCCCCCA						
	2170	2180	2190	2200	2210	2220	2230

**Fig. 27P**

	2210	2220	2230	2240	2250	2260	2270
Hum.	GGGAGAGGCCCGTTAAGCAGAGACAACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGA						
	.....	.....	.....	.....	.....	.....	.....
Mur.	GGGAAAAGGCTCCACTGAGCAGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGA						
	2240	2250	2260	2270	2280	2290	2300
	2280	2290	2300	2310	2320	2330	2340
Hum.	TGTGACGCTGACAACAACCTAGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGG-CCGGGGCTG--C						
	.....	.....	.....	.....	.....	.....	.....
Mur.	CGTAGATGCCGACACAACCATCTGGGCGCCGAAGTGGCTTAAACA-GGGACACAGATCCGCAGCTGAGC						
	2310	2320	2330	2340	2350	2360	2370
	2350	2360	2370	2380	2390	2400	2410
Hum.	GGTGCAGGCACCTGGCCATGCTGGCTGGCGGCCAAGCACAGCCCTGACTAGGATGACAGCAGCAAAA						
	.....	.....	.....	.....	.....	.....	.....
Mur.	AGAGCAAGCCACTGGCCCTTGTGGCTATGC---CAGGCACAG-----TGCCACTCT--						
	2380	2390	2400	2410			2420
	2420	2430	2440	2450	2460	2470	2480
Hum.	AGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGC						
	.....	.....	.....	.....	.....	.....	.....
Mur.	-GACCA-----GGGTAGGAG--GCT-CT-C-CTGCTA-ACGTGTGTCAC-CTACAG-----C						
	2430	2440	2450	2460			

Fig. 27Q

	2490	2500	2510	2520	2530	2540	2550
Hum.	ACAGCAGTCTG-CCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAAACAGGTGGGGCT						
	:: :::: : :::::::::::::: ::::: ::::: :::::						:::::
Mur.	ACC-CAGTAGTCTCCCTGTGGGACTCTCTCTGC-AAGCACATT-----GGGCT						
	2470 2480 2490 2500 2510						
	2560	2570	2580	2590	2600	2610	
Hum.	ACCCCCAGACCTGCTCCTACACTGATA-TTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAG						
	. : :::: :: : . :::: : . :::::::::: ::::: ::::: ::::: ::::: .. ::::						
Mur.	GTCTCCATACCTGTACTTGTGCTGTGACAGGAAGAGCCAGAC-AGGTTTCTTTGATTTTGATTGACCCAA						
	2520 2530 2540 2550 2560 2570 2580						
	2620	2630	2640	2650	2660	2670	2680
Hum.	GGACCT-CCAGAAACACA-GTGTTTCAAGAGATCCTAAATAACCTGCCTGTCCAGGACCTATGGTA						
	: ::::: ::::::::::: : ::::: ::::::::::: :: ::::: ::::: :::::::::::						
Mur.	GAGCCCTGCCCTGTAAACAAACGTGCTCCAGGAGA-CCATGAAAGGTGTGGCTGTCT-GGGATTCTGTGGTG						
	2590 2600 2610 2620 2630 2640 2650						
	2690	2700	2710	2720	2730	2740	2750
Hum.	ATGAACACCAACATCTAAACAATCATATGCTAA-CATGC---CAC--TCCTGGAAACT-CCACTCTGAA						
	: :::: : :::::::::: ::::: . . ::::: : ::::: ::::: ::::: ::::: :::::						
Mur.	ACAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCTCTGCAAACTCCATCCTGAACGCTGTCACTCTAGA						
	2660 2670 2680 2690 2700 2710 2720						

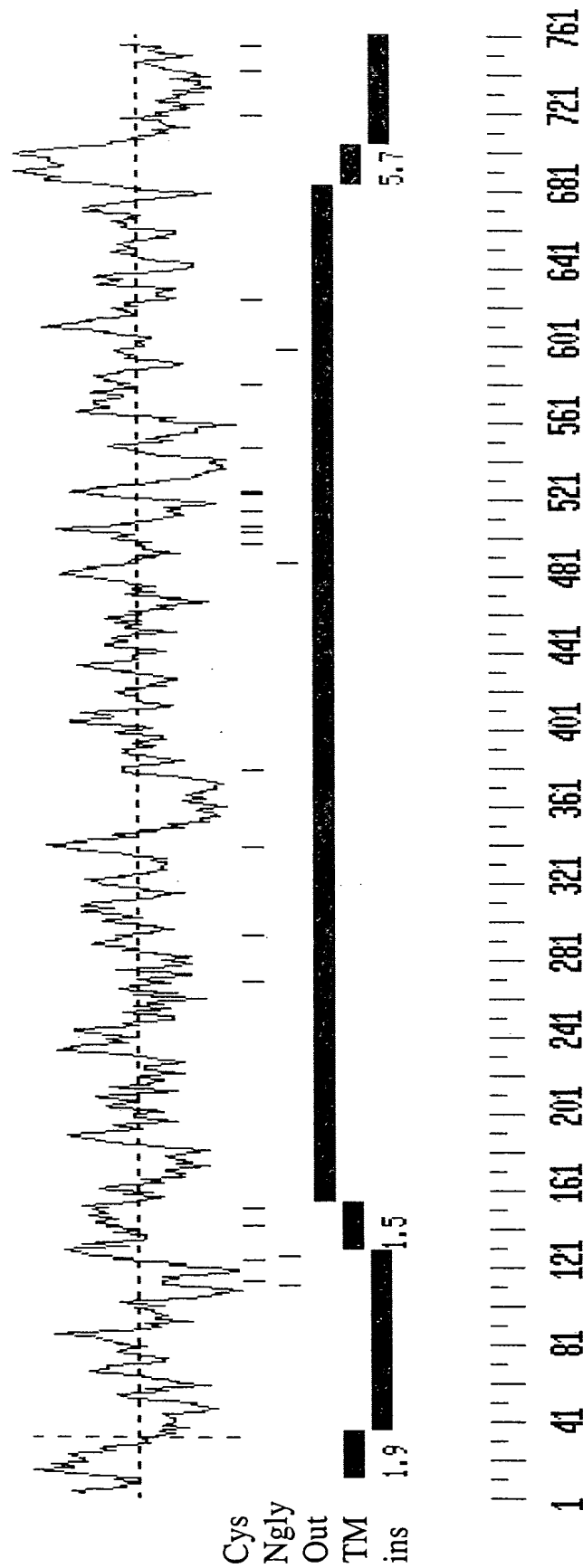
**Fig. 27R**

	2760	2770	2780	2790	2800	2810
Hum.	---GCTGCCGCTTTGGACACCAACACTCCCTTCT-CCCAGG-GTCATGCAGGGATCTGCTCCCTCCTGC					
	2730	2740	2750	2760	2770	2780
Mur.	AGCAGCTGCTGCTTTGAACACACGCCCACCCCTCCTTCCCAAGAGTCTCTATGGAGTTGGC-CCCTTGTGT					
	2820	2830	2840	2850	2860	2870
Hum.	TTCCCTTACCAGTCGTGCACCGCTGACTCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTCTTCTTGC					
	2800	2810	2820	2830	2840	2850
Mur.	TTCCCTTACCAGTCGGGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTAACCACCTTCCCTTCTTGG					
	2890	2900	2910	2920	2930	2940
Hum.	TTCAGTTGGGCAGACTCTGATCCCT---TCTGCCCTGGCAGAATGGCAGGGTAATCTGAGCCTTCTTTC					
	2860	2870	2880	2890	2900	2910
Mur.	TTCAGTTGGACAGATTGTTATTATTGTCCTCTGCCCTGGCTAGAAATGGGGCATAATCTGAGCCTTGTTTC					
	2960	2970	2980	2990	3000	3010
Hum.	ACTCCTTTACCC---TAGCTGACCCCTTCACCTCTCCC--CCCTCCCTTTTCCCTTTGTTTGGGATTCAGA					
	2930	2940	2950	2960	2970	2980
Mur.	---CCTTGTCAGTGTGGCTGACCC-TTGACCTCTTCCCTTCCCTCC---TCCCTTTGTTTGGGATTCAGA					

Fig. 27S







**Fig. 27U**

GTCGACCCACGCGTCCGACGCTTTGGACACTTTCCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCAACTAAAGGA	79
<div style="text-align: center;">M   C   T   K   T   I</div>	
TCAAGAAAGGCCAGCACAGCAGAGATCAGCTGGATCTAGCTCCTGCAGGAG ATG TGT ACA AAG ACA ATC	150
P   V   L   W   G   C   F   L   L   L   W   N   L   Y   V   S   S   S   Q   T   I	26
CCA GTC CTC TGG GGA TGT TTC CTC CTC CTG TGG AAT CTC TAT GTC TCA TCC TCT CAG ACC ATT	210
Y   P   G   I   K   A   R   I   T   Q   R   A   L   D   Y   G   V   Q   A   G	46
TAC CCT GGA ATC AAG GCA AGG ATT ACT CAG AGG GCA CTT GAC TAT GGT GTT CAA GCT GGA	270
M   K   M   I   E   Q   M   L   K   E   K   K   L   P   D   L   S   G   S   E	66
ATG AAG ATG ATT GAG CAA ATG CTA AAA GAA AAG AAA CTC CCA GAT TTA AGC GGT TCT GAG	330
S   L   E   F   L   K   V   D   Y   V   N   Y   N   F   S   N   I   K   I   S	86
TCT CTT GAA TTT CTA AAA GTT GAT TAT GTA AAC TAC AAT TTT TCA AAT ATA AAA ATC AGT	390
A   F   S   F   P   N   T   S   L   A   F   V   P   G   V   G   I   K   A   L	106
GCC TTT TCA TTT CCA AAT ACC TCA TTG GCT TTT GTG CCT GGA GTG GGA ATC AAA GCG CTA	450
T   N   H   G   T   A   N   I   S   T   D   W   G   F   E   S   P   L   F   V	126
ACC AAC CAT GGC ACT GCC AAC ATC AGC ACA GAC TGG GGG TTC GAG TCT CCA CTT TTT GTT	510
L   Y   N   S   F   A   E   P   M   E   K   P   I   L   K   N   L   N   E   M	146
CTG TAT AAC TCC TTT GCT GAG CCC ATG GAG AAA CCC ATT TTA AAG AAC TTA AAT GAA ATG	570

**Fig. 28A**

L	C	P	I	I	A	S	E	V	K	A	L	N	A	N	L	S	T	L	E	166
CTC	TGT	CCC	ATT	ATT	GCA	AGT	GAA	GTC	AAA	GCG	CTA	AAT	GCC	AAC	CTC	AGC	ACA	CTG	GAG	630
V	L	T	K	I	D	N	Y	T	L	L	D	Y	S	L	I	S	S	P	E	186
GTT	TTA	ACC	AAG	ATT	GAC	AAC	TAC	ACT	CTG	CTG	GAT	TAC	TCC	CTA	ATC	AGT	TCT	CCA	GAA	690
I	T	E	N	Y	L	D	L	N	L	K	G	V	F	Y	P	L	E	N	L	206
ATT	ACT	GAG	AAC	TAC	CTT	GAC	CTG	AAC	TTG	AAG	GGT	GTA	TTC	TAC	CCA	CTG	GAA	AAC	CTC	750
T	D	P	P	F	S	P	V	P	F	V	L	P	E	R	S	N	S	M	L	226
ACC	GAC	CCC	CCC	TTC	TCA	CCA	GTT	CCT	TTT	GTG	CTC	CCA	GAA	CGC	AGC	AAC	TCC	ATG	CTC	810
Y	I	G	I	A	E	Y	F	F	K	S	A	S	F	A	H	F	T	A	G	246
TAC	ATT	GGA	ATC	GCC	GAG	TAT	TTC	TTT	AAA	TCT	GCG	TCC	TTT	GCT	CAT	TTC	ACA	GCT	GGG	870
V	F	N	L	T	L	S	T	E	E	I	S	N	H	F	V	Q	N	S	Q	266
GTT	TTC	AAT	CTC	ACT	CTC	TCC	ACC	GAA	GAG	ATT	TCC	AAC	CAT	TTT	GTT	CAA	AAC	TCT	CAA	930
G	L	G	N	V	L	S	R	I	A	E	I	Y	I	L	S	Q	P	F	M	286
GGC	CTT	GGC	AAC	GTG	CTC	TCC	CGG	ATT	GCA	GAG	ATC	TAC	ATC	TTG	TCC	CAG	CCC	TTC	ATG	990
V	R	I	M	A	T	E	P	P	I	I	N	L	Q	P	G	N	F	T	L	306
GTG	AGG	ATC	ATG	GCC	ACA	GAG	CCT	CCC	ATA	ATC	AAT	CTA	CAA	CCA	GGC	AAT	TTC	ACC	CTG	1050
D	I	P	A	S	I	M	M	L	T	Q	P	K	N	S	T	V	E	T	I	326
GAC	ATC	CCT	GCC	TCC	ATC	ATG	ATG	CTC	ACC	CAA	CCC	AAG	AAC	TCC	ACA	GTT	GAA	ACC	ATC	1110

**Fig. 28B**

V	S	M	D	F	V	A	S	T	S	V	G	L	V	I	L	G	Q	R	L	346
GTT	TCC	ATG	GAC	TTC	GTT	GCT	AGT	ACC	AGT	GTT	GGC	CTG	GTT	ATT	TTG	GGA	CAA	AGA	CTG	1170
V	C	S	L	S	L	N	R	F	R	L	A	L	P	E	S	N	R	S	N	366
GTC	TGC	TCC	TTG	TCT	CTG	AAC	AGA	TTC	CGC	CTT	GCT	TTG	CCA	GAG	TCC	AAT	CGC	AGC	AAC	1230
I	E	V	L	R	F	E	N	I	L	S	S	I	L	H	F	G	V	L	P	386
ATT	GAG	GTC	TTG	AGG	TTT	GAA	AAT	ATT	CTA	TCG	TCC	ATT	CTT	CAC	TTT	GGA	GTC	CTC	CCA	1290
L	A	N	A	K	L	Q	Q	G	F	P	L	P	N	P	H	K	F	L	F	406
CTG	GCC	AAT	GCA	AAA	TTG	CAG	CAA	GGA	TTT	CCT	CTG	CCC	AAT	CCA	CAC	AAA	TTT	TTA	TTC	1350
V	N	S	D	I	E	V	L	E	G	F	L	L	I	S	T	D	L	K	Y	426
GTC	AAT	TCA	GAT	ATT	GAA	GTT	CTT	GAG	GGT	TTC	CTT	TTG	ATT	TCC	ACC	GAC	CTG	AAG	TAT	1410
E	T	S	S	K	Q	Q	P	S	F	H	V	W	E	G	L	N	L	I	S	446
GAA	ACA	TCC	TCA	AAG	CAG	CAG	CCA	AGT	TTC	CAC	GTA	TGG	GAA	GGT	CTG	AAC	CTG	ATA	AGC	1470
R	Q	W	R	G	K	S	A	P	*											456
AGA	CAG	TGG	AGG	GGG	AAG	TCA	GCC	CCT	TGA											1500
TTGCCGGTTTGCAATTCA	CCCCAGGAAGTAAATGGTCCTTAATCCTACAACTACTGTAAACCCAGAGGAAAGACAGT	1579																		
ACACACTGGAATTGTAAAGCCCTTGTGAATTGCTTAGGCAGAAAGTTTCTTTAAGCCCTTCAGGAACCCAGAAATAA	1658																			
GGCAGACTCTGTAAAGGGATAAATAGAGGTGTCTGAATGTGAGTGTATGCATGCTGCGTGTCTGTGTTATGTTG	1737																			
TTTGTTTGTTGGGCAAGAAAGATTCTAGGACAAAGAGCTAGGCATGTACTTCTGACCCAGGTGGGTAAGCAACTCTAAG	1816																			

Fig. 28C

TCTGTATTGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTTTCCCCCTACCTGCATATAATTGGTTTTC 1895  
ATGTTTTATATTCACTGTACTATCTTCTCTGTGTTTAAATTAAATTTCTATCAAAAAAAAAAAAAAAAAAAGGGC 1974  
GGCCGC 1980

**Fig. 28D**

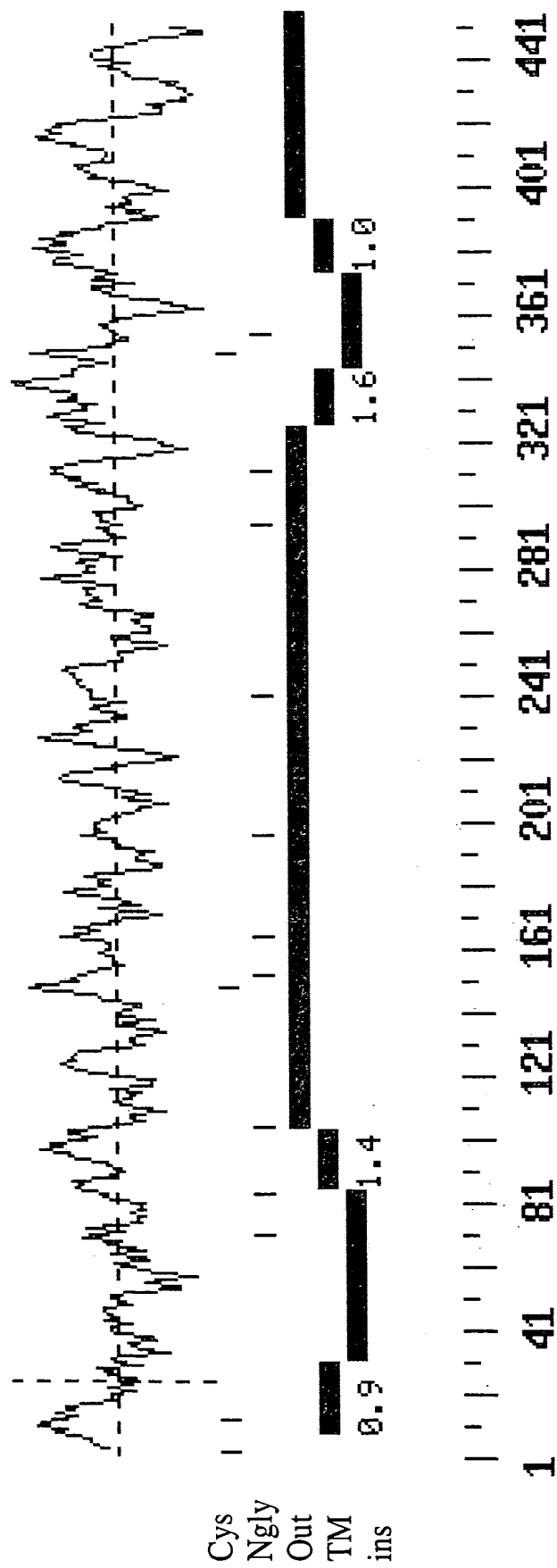


Fig. 28E

```

10      20      30      40      50      60
286 MCTKT-IPVLWGCFL-LWNLVSSSQTIYPGIKARITQRALDYGVAQGMKMIQMLKEKKLPDLSGSESL
:      :      :      :      :      :      :      :      :      :      :
BPI MARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS--DSF
10      20      30      40      50      60

70      80      90      100     110     120     130
286 EFLKVDYVNYNFSNIKISAFSPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME--
:      :      :      :      :      :      :      :      :      :      :
BPI KIKHLGKGHYSFYMDIREFQLPSSQISMVNPVGLKFISNANIKISGKWKAKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130

286 -----KPI-----140      150
:      :      :      :      :      :      :      :      :      :      :
BPI SISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS
140     150     160     170     180     190     200

160     170     180     190     200     210     220
286 VKA-LNANLSTLEVLTKIDNYTLDDYSLISSPEITENYLDNLKGVFYPLENLTDPFSPVFLPERSN
:      :      :      :      :      :      :      :      :      :      :
BPI VSSKLQPYFQTLFVMTKIDSVAGINYLVAAPPATTAETLDVQMKGEFYSENHHNPPFPFAPVMEFFAAHD
210     220     230     240     250     260     270

```

Fig. 28F



[illegible]

```

10      20      30      40      50      60
286 MCTKTIPVLWGCFLLNLYVSSQTI--YPGIKARITQRALDYGVOAGMKMIEQMLKEKKLPDLGSESL
: . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP MGALARAL--PSILLALLTSTPEALGANPGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTG--DL
10      20      30      40      50      60
70      80      90      100     110     120     130
286 EFLKVDYVNYNFSNIKISAFSPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLVNSFAEPME--
. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP RIPHVGRGRYEFHSLNIHEFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGM
70      80      90      100     110     120     130
286 -----KPI-----LKN-LNEMLCPIIASE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP SISADLKLGSNPTSGKPTITCSCSCSSHINSVHVHISKVKWGLIQLFHKKIESALRNKMNSQVCEKVTNS
140     150     160     170     180     190     200
160     170     180     190     200     210     220
286 VKA-LNANLSTLEVLTKIDNYTLLDYSLISSPEITENYLDNLKGVFYPLENLTDPFSPVFFVLPERSON
: . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RENP VSSKLQPYFQTLPMVMTKIDSVAGINYGVLVAPPATTAETLDVQMKGEFYSENHHNPPPPFAPPVMEFFPAAHD
210     220     230     240     250     260     270

```

[illegible]

**Fig. 28I**

GTCGACCCACGCGTCCGGGAATTGCAGCAGGAAATATGTGAAGAGTTTTTAAACCCACAAAATTCTTCTTACTTTAGA	79
M L E T L S R Q	
ATTAGTTGTTACATTGCAGGAAAAATAATGCAGATGTTGGACC ATG TTG GAA ACC TTG TCA AGA CAG	8 149
W I V S H R M E M W L L I L V A Y M F Q	28
TGG ATT GTC TCA CAC AGA ATG GAA ATG TGG CTT CTG ATT CTG GTG GCG TAT ATG TTC CAG	209
R N V N S V H M P T K A V D P E A F M N	48
AGA AAT GTG AAT TCA GTA CAT ATG CCA ACT AAA GCT GTG GAC CCA GAA GCA TTC ATG AAT	269
I S E I I Q H Q G Y P C E E Y E V A T E	68
ATT AGT GAA ATC ATC CAA CAT CAA GGC TAT CCC TGT GAG GAA TAT GAA GTC GCA ACT GAA	329
D G Y I L S V N R I P R G L V Q P K K T	88
GAT GGG TAT ATC CTT TCT TCT AAC AGG ATT CCT CGA GGC CTA GTG CAA CCT AAG AAG ACA	389
G S R P V V L L Q H G L V G A S N W I	108
GGT TCC AGG CCT GTG GTG TTA CTG CAG CAT GGC CTA GTT GGA GGT GCT AGC AAC TGG ATT	449
S N L P N N S L G F I L A D A G F D V W	128
TCC AAC CTG CCC AAC AAT AGC CTG GGC TTC ATT CTG GCA GAT GCT GGT TTT GAC GTG TGG	509
M G N S R G N A W S R K H K T L S I D Q	148
ATG GGG AAC AGC AGG GGA AAC GCC TGG TCT CGA AAA CAC AAG ACA CTC TCC ATA GAC CAA	569

**Fig. 29A**

D	E	F	W	A	F	S	Y	D	E	M	A	R	F	D	L	P	A	V	I	168
GAT	GAG	TTC	TGG	GCT	TTC	AGT	TAT	GAT	GAG	ATG	GCT	AGG	TTT	GAC	CTT	CCT	GCA	GTG	ATA	629
N	F	I	L	Q	K	T	G	Q	E	K	I	Y	Y	V	G	Y	S	Q	G	188
AAC	TTT	ATT	TTG	CAG	AAA	ACG	GGC	CAG	GAA	AAG	ATC	TAT	TAT	GTC	GGC	TAT	TCA	CAG	GGC	689
T	T	M	G	F	I	A	F	S	T	M	P	E	L	A	Q	K	I	K	M	208
ACC	ACC	ATG	GGC	TTT	ATT	GCA	TTT	TCC	ACC	ATG	CCA	GAG	CTG	GCT	CAG	AAA	ATC	AAA	ATG	749
Y	F	A	L	A	P	I	A	T	V	K	H	A	K	S	P	G	T	K	F	228
TAT	TTT	GCT	TTA	GCA	CCC	ATA	GCC	ACT	GTT	AAG	CAT	GCA	AAA	AGC	CCC	GGG	ACC	AAA	TTT	809
L	L	L	P	D	M	M	I	K	G	L	F	G	K	K	E	F	L	Y	Q	248
TTG	TTG	CTG	CCA	GAT	ATG	ATG	ATC	AAG	GGA	TTG	TTT	GGC	AAA	AAA	GAA	TTT	CTG	TAT	CAG	869
T	R	F	L	R	Q	L	V	I	Y	L	C	G	Q	V	I	L	D	Q	I	268
ACC	AGA	TTT	CTC	AGA	CAA	CTT	GTT	ATT	TAC	CTT	TGT	GGC	CAG	GTG	ATT	CTT	GAT	CAG	ATT	929
C	S	N	I	M	L	L	L	G	G	F	N	T	N	N	M	N	M	S	R	288
TGT	AGT	AAT	ATC	ATG	TTA	CTT	CTG	GGT	GGA	TTC	AAC	ACC	AAC	AAT	ATG	AAC	ATG	AGC	CGA	989
A	S	V	Y	A	A	H	T	L	A	G	T	S	V	Q	N	I	L	H	W	308
GCA	AGT	GTA	TAT	GCT	GCC	CAC	ACT	CTT	GCT	GGA	ACA	TCT	GTG	CAA	AAT	ATT	CTA	CAC	TGG	1049
S	Q	A	V	N	S	G	E	L	R	A	F	D	W	G	S	E	T	K	N	328
AGC	CAG	GCA	GTG	AAT	TCT	GGT	GAA	CTC	CGG	GCA	TTT	GAC	TGG	GGG	AGT	GAG	ACC	AAA	AAT	1109

**Fig. 29B**

L	E	K	C	N	Q	P	T	P	V	R	Y	R	V	R	D	M	T	V	P	348
CTG	GAA	AAA	TGC	AAT	CAG	CCA	ACT	CCT	GTA	AGG	TAC	AGA	GTC	AGA	GAT	ATG	ACG	GTC	CCT	1169
T	A	M	W	T	G	G	Q	D	W	L	S	N	P	E	D	V	K	M	L	368
ACA	GCA	ATG	TGG	ACA	GGA	GGT	CAG	GAC	TGG	CTT	TCA	AAT	CCA	GAA	GAC	GTG	AAA	ATG	CTG	1229
L	S	E	V	T	N	L	I	Y	H	K	N	I	P	E	W	A	H	V	D	388
CTC	TCT	GAG	GTG	ACC	AAC	CTC	ATC	TAC	CAT	AAG	AAT	ATT	CCT	GAA	TGG	GCT	CAC	GTG	GAT	1289
F	I	W	G	L	D	A	P	H	R	M	Y	N	E	I	I	H	L	M	Q	408
TTC	ATC	TGG	GGT	TTG	GAT	GCT	CCT	CAC	CGT	ATG	TAC	AAT	GAA	ATC	ATC	CAT	CTG	ATG	CAG	1349
Q	E	E	T	N	L	S	Q	G	R	C	E	A	V	L	*					424
CAG	GAG	GAG	ACC	AAC	CTT	TCC	CAG	GGA	CGG	TGT	GAG	GCC	GTA	TTG	TGA					1397
AGCATCTGACACTGACGATCTTTAGGACAAACCTCCTGAGGGATGGGGCTAGGACCCCATGAAGGCAGAAATTACGGAGAGCA	1476																			
GAGACCTAGTATACATTTTTCAGATTCCCTGCACCTTGGCATAAATCCGACACTTACATTTACATTTTCTGTGATAA	1555																			
TTAAAGTACTTATTAGGTAAATAGAGGTTTTGTATGCTATTATATATCTCTTTAAACACACCTATTGTTTTTCTATAAGCCAT	1634																			
AGCCAGAAAATATCTAGACATTCTCTATATCATTCAGGTAAATCTCTTTAAACACACCTATTGTTTTTCTATAAGCCAT	1713																			
ATTTTGGAGCACTAAAGTAAATGGCAAAATGGGACAGATATTGAGGCTGGAGTCTGTGGATTATTGTTGACTTTGA	1792																			
CAAAATAAGCTAGACATTTTCACCTTGTGTCACAGACATAAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA	1871																			
CAACAACAAATCAGTGTACAGTATGGATGAAATCTATGTTAAGCATTTCTCAGAAATAAGGCCAAGTTTTTATAGTTGCA	1950																			
TCTCAGGGGAAGAAAATTTTATAGGATGTTTATGAGTTCTCCAATAAAATGCATTCTGCATTACATAAAAAA	2029																			
AAAAAGGGCGCCGC	2044																			

Fig. 29C

	10	20	30	40	50	60	70
294	MLETLSRQWIVSHRMEMWLLILVAYMFQNNVNSVHMPTKAVDPEAFMNISEIIHQGYPCEEYEVATEDG						
:	...	:	:	:	:	:	:
HLP	M-----WLL---	LTMASLISVLGTTGHLFGKLIH----	PGSPEVTMNISQMITYWGYPNEEYEVVATEDG				
	10	20	30	40	50		
	80	90	100	110	120	130	140
294	YILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNWSRK						
:	:	:	:	:	:	:	:
HLP	YILEVNRIPYGKKNSGNTGQRPVVFLQHGLLASATNWISNLPNNSLAFILADAGYDVWLGNSRGNTWARR						
	60	70	80	90	100	110	120
	150	160	170	180	190	200	210
294	HKTLSIDQDEFWAFSYDEMARFDLPAVINFILQKTQEKIYVVGYSQGTMGFIAFSTMPELAQIKMYF						
:	:	:	:	:	:	:	:
HLP	NLYYSPDSVEFWAFSFDDEMAKYDLPATIDFIVKKTGQKQLHYVGHVSQGTIGFIAFSTNPSLAKRIKTFY						
	130	140	150	160	170	180	190
	220	230	240	250	260	270	
294	ALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQ-LVIYLCGQVILDQICSNIMLLLGGF						
:	:	:	:	:	:	:	:
HLP	ALAPVATVKYTKSLINKLRFVPQSLFKFIFGDKIF-YPHNFFDQFLATEVCSREMLNLLCSNALFIICGF						
	200	210	220	230	240	250	260

**Fig. 29D**

```

280      290      300      310      320      330      340
294 NTNNMMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVPT
... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP DSKNFNTSRLLDVYLSHNPAGTSVQNMFWHTQAVKSGKFAQYDWGSPVQNRMHYDQSQPPYNNVTAMNVPI
270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 AMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HLP AVWNGGKDLLADPPQDVGLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK-----
340      350      360      370      380      390

420
294 EAVL

HLP ----

```

Fig. 29E



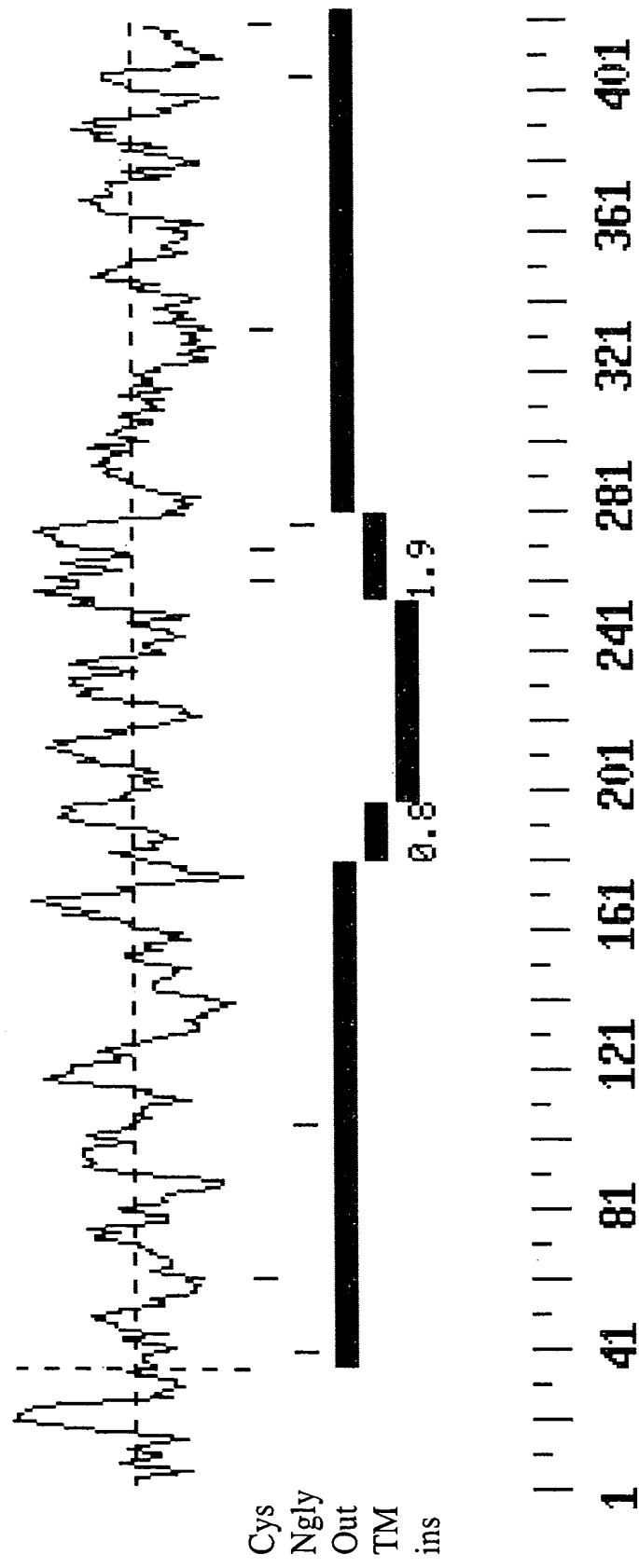


Fig. 29F

```

10      20      30      40      50      60
294 MLETLRQWIVSHRMEMWLLILVAYMFQNNVNSVHMPK--AVDPEAFMNISEIIQHQQYPCPEEYEVATE
:      :...: . . . . :      :      :      :      :      :      :
LAL M-----KMRFLGLVVCLVPLHSEGGKLTAVDPETNMNVSEIISYWGFPSSEYYLVETE
      10      20      30      40      50

70      80      90      100     110     120     130
294 DGYILSVNRIPRGLVQPKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNAWS
:      :      : . . . . . :      :      :      :      :      :
LAL DGYILCLNRI PHGRKNHSDKGPVVF LQHGLLADSSNWVTNLANSSLGFILADAGFDVWMGNSRGNTWS
      60      70      80      90      100     110     120

140     150     160     170     180     190     200
294 RKHKTLSIDQDEFWAFSYDEMAREFDLP AVINFILQKTGQEKIYVVGYSQGTMGFLAFSTMPELAQKIKM
:      :      :      :      :      :      :      :      :
LAL RKHKTLVSQDEFWAFSYDEMAKYDLPASINFILNKTGQEQVYVVGHSQGTTFIAFSQIPELAKRIKM
      130     140     150     160     170     180     190

210     220     230     240     250     260     270
294 YFALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLLGG
:      :      : . . . . . :      :      :      :      :      :
LAL FFALGPVASVAFCTSPMAKLGRLPDHLIKDLFGDKFELPQSAFLKWLGTHVTHVILKELCGNLCFLLCG
      200     210     220     230     240     250     260

```

**Fig. 29G**

```

280      290      300      310      320      330      340
294 FNTNNMMSRASVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDMTVP
   :: :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL FNERNLNMSRVDVYTTHTSPAGTSVQNMLHWSQAVKFKQAFDWSGSAKNYFHYNQSYPPTYNVKDMMLVP
270      280      290      300      310      320      330

350      360      370      380      390      400      410
294 TAMWTGGQDWLSNPEDVKMLLSEVTNLIYHKNIPEWAHVDFIWGLDAPHRMYNEIIHLMQQEETNLSQGR
   :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
LAL TAVWSSGGHDWLADVVDVNILLTQITNLFHESIPWEHLDFIWGLDAPWRLYNKIIINLMRKYQ-----
340      350      360      370      380      390

420
294 CEAVL

LAL -----

```

**Fig. 29H**

GTCGACCCACGCGTCCACGGCAGGGCTCCCGGGCGCAGCATTGCCCCCCCCTGCACCACTCACCAAG	ATG	GCT	75
T L G H T F P F Y A G P K P T F P M D T			22
ACT TTG GGA CAC ACA TTC CCC TTC TAT GCT GGC CCC AAG CCA ACC TTC CCG ATG GAC ACC			135
T L A S I I M I F L T A L A T F I V I L			42
ACT TTG GCC AGC ATC ATC ATG ATC TTT CTG ACT GCA CTG GCC ACG TTC ATC GTC ATC CTG			195
P G I R G K T R L F W L L R V V T S L F			62
CCT GGC ATT CGG GGA AAG ACG AGG CTG TTC TGG CTG CTT CGG GTG GTG ACC AGC TTA TTC			255
I G A A I L A V N F S S E W S V G Q V S			82
ATC GGG GCT GCA ATC CTG GCT GTG AAT TTC AGT TCT GAG TGG TCT GTG GGC CAG GTC AGC			315
T N T S Y K A F S S E W I S A D I G L Q			102
ACC AAC ACA TCA TAC AAG GCC TTC AGT TCT GAG TGG ATC AGC GCT GAT ATT GGG CTG CAG			375
V G L G G V N I T L T G T P V Q Q L N E			122
GTC GGG CTG GGT GGA GTC AAC ATC ACA CTC ACA GGG ACC CCC GTG CAG CAG CTG AAT GAG			435
T I N Y N E E F T W R L G E N Y A E E C			142
ACC ATC AAT TAC AAC GAG GAG TTC ACC TGG CGC CTG GGT GAG AAC TAT GCT GAG GAG TGT			495
A K A L E K G L P D P V L Y L A E K F T			162
GCA AAG GCT CTG GAG AAG GGG CTG CCA GAC CCT GTG TTG TAC CTA GCT GAG AAG TTC ACT			555

**Fig. 30A**

P	R	S	P	C	G	L	Y	R	Q	Y	R	L	A	G	H	Y	T	S	A	182	
CCA	AGA	AGC	CCA	TGT	GGC	CTA	TAC	TAC	CGC	CAG	TAC	CGC	CTG	GCG	GGA	CAC	TAC	ACC	TCA	GCC	615
M	L	W	V	A	F	L	C	W	L	L	A	N	V	M	L	S	M	P	V	202	
ATG	CTA	TGG	GTG	GCA	TTC	CTC	TGC	TGG	CTG	CTG	GCC	AAT	GTG	ATG	CTC	TCC	ATG	CCT	GTG	675	
L	V	Y	G	G	Y	M	L	L	A	T	G	I	F	Q	L	L	A	L	L	222	
CTG	GTA	TAT	GGT	GGC	TAC	ATG	CTA	TTG	GCC	ACG	GGC	ATC	TTC	CAG	CTG	TTG	GCT	CTG	CTC	735	
F	F	S	M	A	T	S	L	T	S	P	C	P	L	H	L	G	A	S	V	242	
TTC	TTC	TCC	ATG	GCC	ACA	TCA	CTC	ACC	TCA	CCC	TGT	CCC	CTG	CAC	CTG	GGC	GCT	TCT	GTG	795	
L	H	T	H	H	G	P	A	F	W	I	T	L	T	T	G	L	L	C	V	262	
CTG	CAT	ACT	CAC	CAT	GGG	CCT	GCC	TTC	TGG	ATC	ACA	TTG	ACC	ACA	GGA	CTG	CTG	TGT	GTG	855	
L	L	G	L	A	M	A	V	A	H	R	M	Q	P	H	R	L	K	A	F	282	
CTG	CTG	GGC	CTG	GCT	ATG	GCG	GTG	GCC	CAC	AGG	ATG	CAG	CCT	CAC	AGG	CTG	AAG	GCT	TTC	915	
F	N	Q	S	V	D	E	D	P	M	L	E	W	S	P	E	E	G	G	L	302	
TTC	AAC	CAG	AGT	GTG	GAT	GAA	GAC	CCC	ATG	CTG	GAG	TGG	AGT	CCT	GAG	GAA	GGT	GGA	CTC	975	
L	S	P	R	Y	R	S	M	A	D	S	P	K	S	Q	D	I	P	L	S	322	
CTG	AGC	CCC	CGC	TAC	CGG	TCC	ATG	GCT	GAC	AGT	CCC	AAG	TCC	CAG	GAC	ATT	CCC	CTG	TCA	1035	
E	A	S	S	T	K	A	Y	C	K	E	A	H	P	K	D	P	D	C	A	342	
GAG	GCT	TCC	TCC	ACC	AAG	GCA	TAC	TGT	AAG	GAG	GCA	CAC	CCC	AAA	GAT	CCT	GAT	TGT	GCT	1095	

**Fig. 30B**

L	*	344
TTA	TAA	1101
CATTCCTCCCGTGGAGGCCACCTGGACTTCCAGTCTGGCTCCAAACCTCATTTGGCGCCCCATAAAACCAGCAGAACTG		1180
CCCTCAGGGTGGCTGTTACCAAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAGGAGGCTCTATATACTGATGTT		1259
AAAAACAAAACAAAACAAAAGCCCTAAGGAC'TGAAGAGATGCTGGCCCTGTCCATAAAGCCCTGTTGCCATGATAAG		1338
GCCAAGCAGGGCTAGCTTATCTGCACAGCAACCCAGCCTTCCGTGCTGCCCTTGCCCTCTTCAAGATGCTATTCACTGA		1417
AACCTAACTTCAACCCCATAAACACAGCAGGTGGGGTTACATAATGATTTCTCCATATGGTTTCCCTCATCCCTCGGCA		1496
CCCTTGTTTTCCTTTTCCCTGGGTTCCCTTTTGTTCTTCTTACTTCTCCAGCTTGTGTGGCCCTTTTGGTACAATGAA		1575
AGACAGCACTGGAAGGAGGGGAAACCAAC'TTCTCATCCTAGGCTAAACATTAAACCAACTATGCCACATTCTCTTTGA		1654
GCTTCAGTTCCCAAATTTGCTACATAAGATTGCAAGACTTGCCCAAGAAATCTTGGGATTTATCTTTCATGCCCTTGCTGA		1733
CACCTACCTTGGCCCTCAAACACACCTCACAGAAGCCAGGTGGGAAGTAGGGAATCAACTCCAACGCTATTCTT		1812
TCCCACCCCACTCAGCTGGGCTAGCTGAGTGGCATCCAGGACGGGGAGTGGGTGACCTGCCCTCATCACTGCCACCTAA		1891
CGTCCCCCTGGGTGGTTCAGAAAGATGCTAGCTCTGGTAGGGTCCCTCCGGCCCTCACTAGAGGGCCCCCTATTACTC		1970
TGGAGTCGACGCAGAGAAATCAGGTTTTCACAGCACTGCGGAGAGTGTACTAGGCTGTCTCCAGCCAGCGAAGCTCATGA		2049
GGACGTGCGACCCCGCGGAGAAAGCCATGAAAATTAATGGGAAAAAACAGTTTTTAAAAAATAAAAGGGCG		2128
GCCGC		2133

**Fig. 30C**

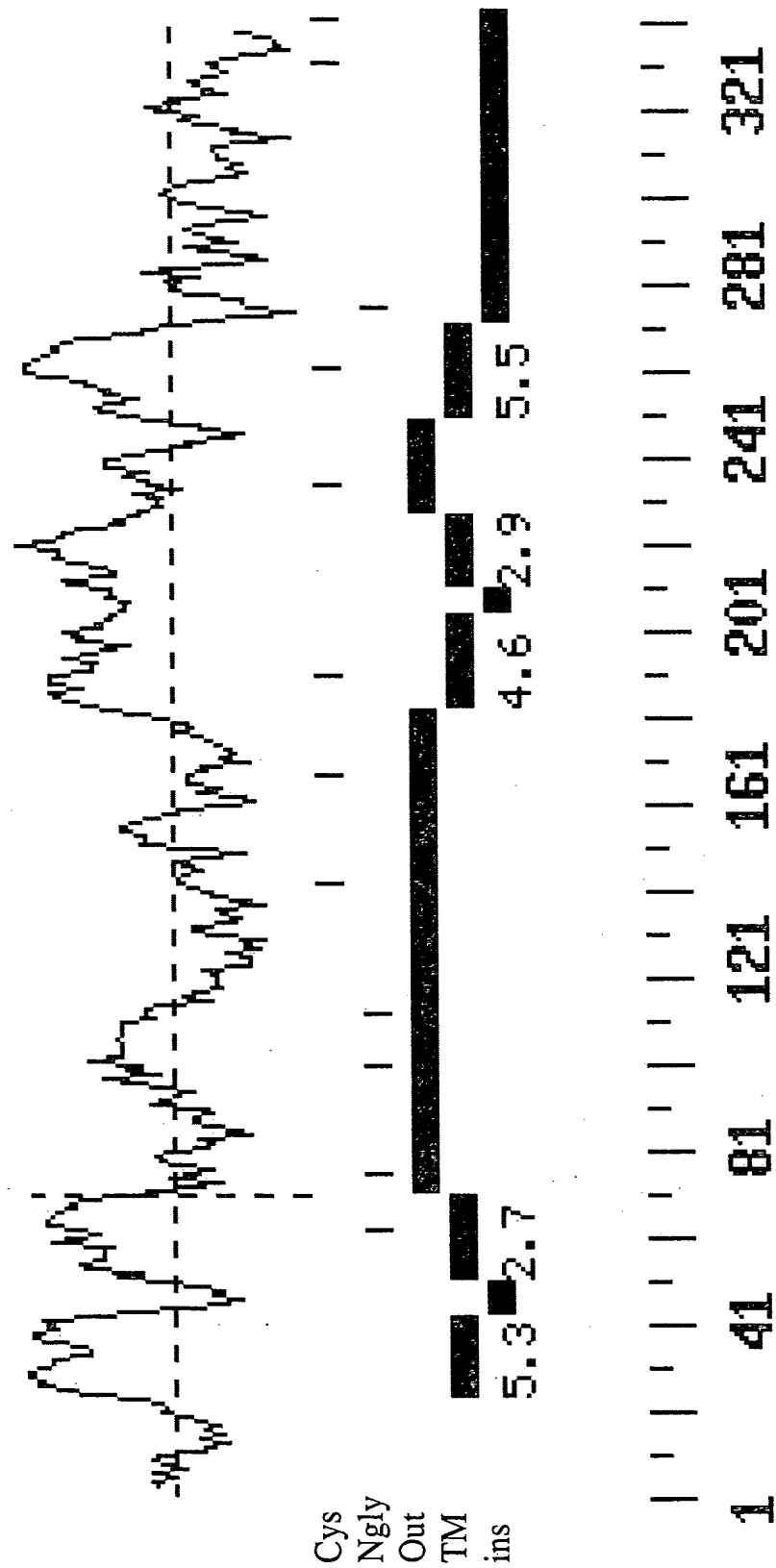


Fig. 30D

	10	20	30	40	50	60	70
296	MATLGH	TFPYAGPKPT	FTL	ASIMIFL	TALATF	IVILPGIR	GKTRLFWLLRVV
	:	:	:	:	:	:	:
CRP	M-RIAH	-----ASSR	GN	-----SIFS	VFLIPLIA	YILILPGVR	-RKRVT
	10	20	30	40	50		
	80	90	100	110	120	130	
296	NFSSEW	SVGQVSTNT	SYKAFS	SEWISAD	IGLQVGLG	VNITL	-----TGTP
	:	:	:	:	:	:	:
CRP	LIYPCW	ASGSQMI	YTQFR	GHSNER	ILAKIG	VEIGLQ	KVNVTLKFER
	60	70	80	90	100	110	120
	140	150	160	170	180	190	200
296	RLGENY	AEECAK	LEKGLP	DPVLYL	AEKFT	-PRSPC	GLYRQYRL
	:	:	:	:	:	:	:
CRP	SGISSM	AEALHH	GLENG	LPYPML	SVLE	YFSLNQ	DSFDWGR
	130	140	150	160	170	180	190
	210	220	230	240	250	260	
296	PVLVYG	GMYML	LATG	IFQL	LALLFF	SMATSL	TSPCPLHL
	:	:	:	:	:	:	:
CRP	PHNAYK	S--ILAT	GISCL	IACLV	YL---LL	SPCEL	RIAF
	200	210	220	230	240	250	260

Fig. 30E



```

270      280      290      300      310      320
296 LGLAMAVAHRMQPHRLKAFNQSVDEDPMLEW-----SPEEGLLSPRY--RSMADSPKSQDIPLSEAS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CRP CGLGLGICEHWRIYTLSTFLDASLDEHVGPWKKKLPTGGPALQGVQIGAYGTNTTNSRRDKNDISSDKTA
270      280      290      300      310      320      330

330
296 STKAY-----CK-----EAHPKDPD-----CA----L
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CRP GSSGFQSRSTCQSSASSASLRSQSSIETVHDEAELEERTHVHFLQEPCCSSSST
340      350      360      370      380

```

**Fig. 30F**